



wwPDB EM Validation Summary Report ⓘ

Mar 2, 2025 – 10:42 PM EST

PDB ID : 9DOG
EMDB ID : EMD-47083
Title : Octahedral small virus-like particles of dengue virus type 2 (octahedral reconstruction)
Authors : Johnson, A.; Dodes Traian, M.; Walsh, R.M.; Jenni, S.; Harrison, S.C.
Deposited on : 2024-09-19
Resolution : 6.50 Å(reported)
Based on initial model : .

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

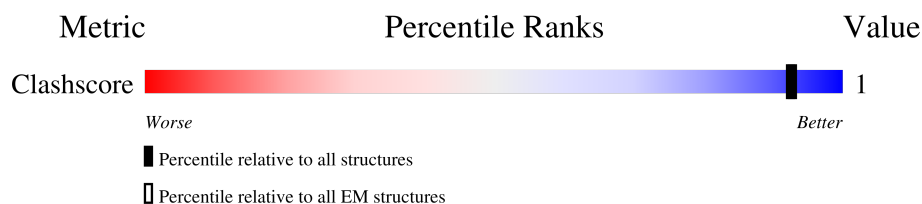
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


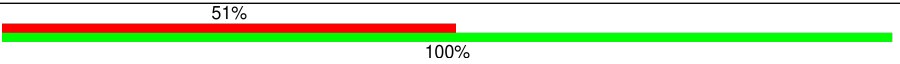
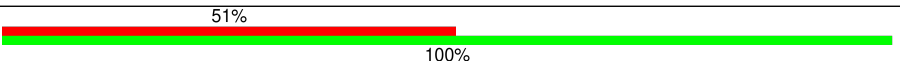
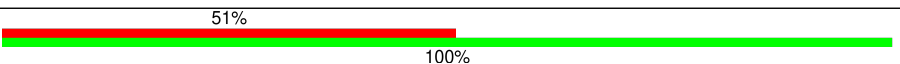
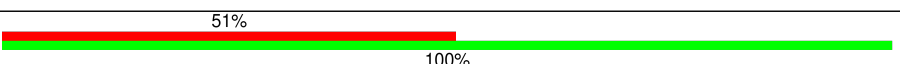
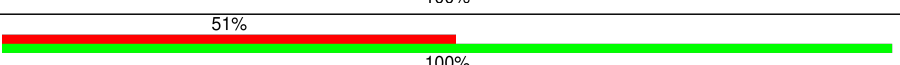
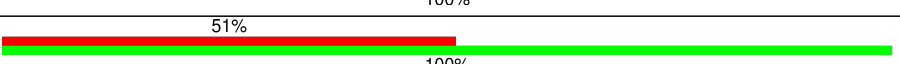
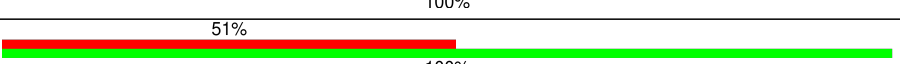
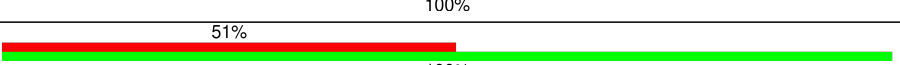
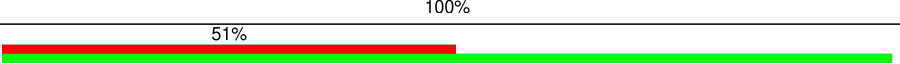
The reported resolution of this entry is 6.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A000	495	
1	A001	495	
1	A002	495	
1	A003	495	
1	A004	495	
1	A005	495	
1	A006	495	
1	A007	495	
1	A008	495	
1	A009	495	

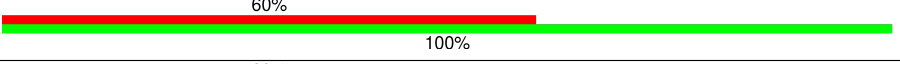
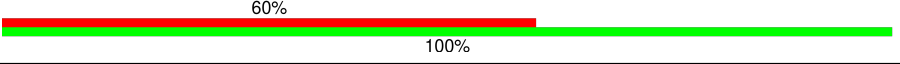

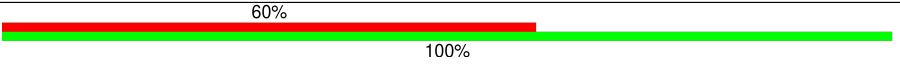
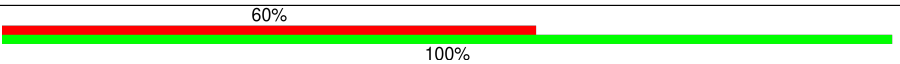
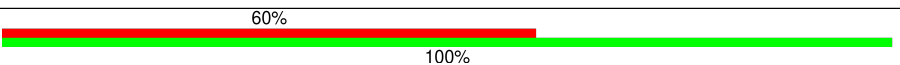

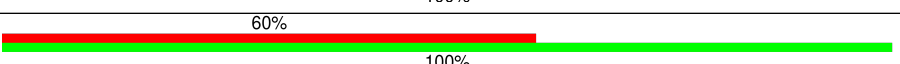
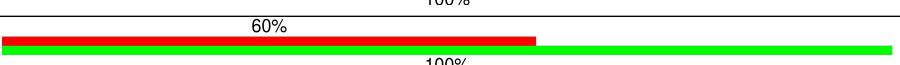
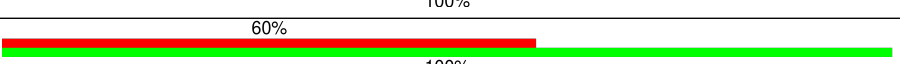
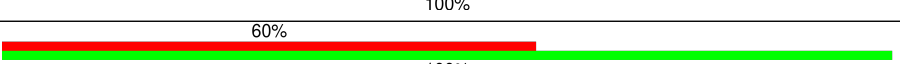

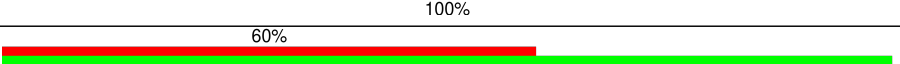


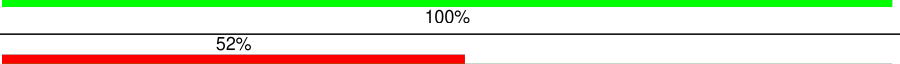

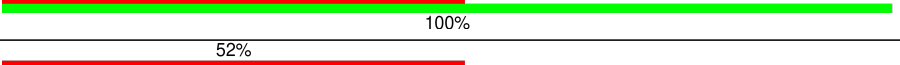
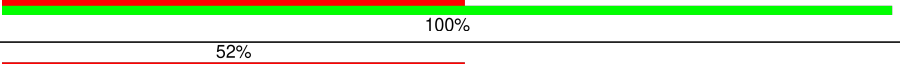
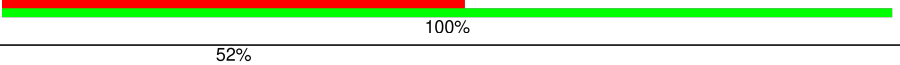
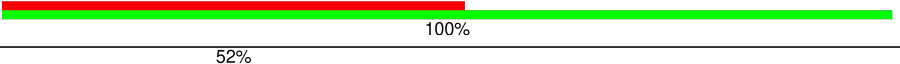
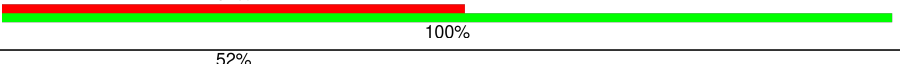
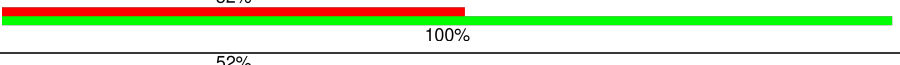
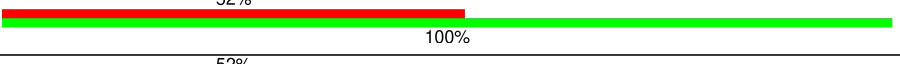
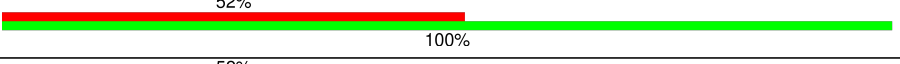
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	A010	495	51% 100%
1	A011	495	51% 100%
1	A012	495	51% 100%
1	A013	495	51% 100%
1	A014	495	51% 100%
1	A015	495	51% 100%
1	A016	495	51% 100%
1	A017	495	51% 100%
1	A018	495	51% 100%
1	A019	495	51% 100%
1	A020	495	51% 100%
1	A021	495	51% 100%
1	A022	495	51% 100%
1	A023	495	51% 100%
1	B000	495	60% 100%
1	B001	495	60% 100%
1	B002	495	60% 100%
1	B003	495	60% 100%
1	B004	495	60% 100%
1	B005	495	60% 100%
1	B006	495	60% 100%
1	B007	495	60% 100%
1	B008	495	60% 100%
1	B009	495	60% 100%
1	B010	495	60% 100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	B011	495	60% 
1	B012	495	60% 
1	B013	495	60% 
1	B014	495	60% 
1	B015	495	60% 
1	B016	495	60% 
1	B017	495	60% 
1	B018	495	60% 
1	B019	495	60% 
1	B020	495	60% 
1	B021	495	60% 
1	B022	495	60% 
1	B023	495	60% 
1	C000	495	52% 
1	C001	495	52% 
1	C002	495	52% 
1	C003	495	52% 
1	C004	495	52% 
1	C005	495	52% 
1	C006	495	52% 
1	C007	495	52% 
1	C008	495	52% 
1	C009	495	52% 
1	C010	495	52% 
1	C011	495	52% 

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	C012	495	<div>52%</div> <div>100%</div>
1	C013	495	<div>52%</div> <div>100%</div>
1	C014	495	<div>52%</div> <div>100%</div>
1	C015	495	<div>52%</div> <div>100%</div>
1	C016	495	<div>52%</div> <div>100%</div>
1	C017	495	<div>52%</div> <div>100%</div>
1	C018	495	<div>52%</div> <div>100%</div>
1	C019	495	<div>52%</div> <div>100%</div>
1	C020	495	<div>52%</div> <div>100%</div>
1	C021	495	<div>52%</div> <div>100%</div>
1	C022	495	<div>52%</div> <div>100%</div>
1	C023	495	<div>52%</div> <div>100%</div>
2	D000	166	<div>80%</div> <div>100%</div>
2	D001	166	<div>80%</div> <div>100%</div>
2	D002	166	<div>80%</div> <div>100%</div>
2	D003	166	<div>80%</div> <div>100%</div>
2	D004	166	<div>80%</div> <div>100%</div>
2	D005	166	<div>80%</div> <div>100%</div>
2	D006	166	<div>80%</div> <div>100%</div>
2	D007	166	<div>80%</div> <div>100%</div>
2	D008	166	<div>80%</div> <div>100%</div>
2	D009	166	<div>80%</div> <div>100%</div>
2	D010	166	<div>80%</div> <div>100%</div>
2	D011	166	<div>80%</div> <div>100%</div>
2	D012	166	<div>80%</div> <div>100%</div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D013	166	80% 100%
2	D014	166	80% 100%
2	D015	166	80% 100%
2	D016	166	80% 100%
2	D017	166	80% 100%
2	D018	166	80% 100%
2	D019	166	80% 100%
2	D020	166	80% 100%
2	D021	166	80% 100%
2	D022	166	80% 100%
2	D023	166	80% 100%
2	E000	166	84% 100%
2	E001	166	84% 100%
2	E002	166	84% 100%
2	E003	166	84% 100%
2	E004	166	84% 100%
2	E005	166	84% 100%
2	E006	166	84% 100%
2	E007	166	84% 100%
2	E008	166	84% 100%
2	E009	166	84% 100%
2	E010	166	84% 100%
2	E011	166	84% 100%
2	E012	166	84% 100%
2	E013	166	84% 100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E014	166	<div>84%</div> <div>100%</div>
2	E015	166	<div>84%</div> <div>100%</div>
2	E016	166	<div>84%</div> <div>100%</div>
2	E017	166	<div>84%</div> <div>100%</div>
2	E018	166	<div>84%</div> <div>100%</div>
2	E019	166	<div>84%</div> <div>100%</div>
2	E020	166	<div>84%</div> <div>100%</div>
2	E021	166	<div>84%</div> <div>100%</div>
2	E022	166	<div>84%</div> <div>100%</div>
2	E023	166	<div>84%</div> <div>100%</div>
2	F000	166	<div>84%</div> <div>100%</div>
2	F001	166	<div>84%</div> <div>100%</div>
2	F002	166	<div>84%</div> <div>100%</div>
2	F003	166	<div>84%</div> <div>100%</div>
2	F004	166	<div>84%</div> <div>100%</div>
2	F005	166	<div>84%</div> <div>100%</div>
2	F006	166	<div>84%</div> <div>100%</div>
2	F007	166	<div>84%</div> <div>100%</div>
2	F008	166	<div>84%</div> <div>100%</div>
2	F009	166	<div>84%</div> <div>100%</div>
2	F010	166	<div>84%</div> <div>100%</div>
2	F011	166	<div>84%</div> <div>100%</div>
2	F012	166	<div>84%</div> <div>100%</div>
2	F013	166	<div>84%</div> <div>100%</div>
2	F014	166	<div>84%</div> <div>100%</div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F015	166	<div><div>84%</div><div>100%</div></div>
2	F016	166	<div><div>84%</div><div>100%</div></div>
2	F017	166	<div><div>84%</div><div>100%</div></div>
2	F018	166	<div><div>84%</div><div>100%</div></div>
2	F019	166	<div><div>84%</div><div>100%</div></div>
2	F020	166	<div><div>84%</div><div>100%</div></div>
2	F021	166	<div><div>84%</div><div>100%</div></div>
2	F022	166	<div><div>84%</div><div>100%</div></div>
2	F023	166	<div><div>84%</div><div>100%</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 47592 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called glycoprotein E.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A000	495	Total C 495 495	0	495
1	C004	495	Total C 495 495	0	495
1	A005	495	Total C 495 495	0	495
1	B005	495	Total C 495 495	0	495
1	C005	495	Total C 495 495	0	495
1	A006	495	Total C 495 495	0	495
1	B006	495	Total C 495 495	0	495
1	C006	495	Total C 495 495	0	495
1	A007	495	Total C 495 495	0	495
1	B007	495	Total C 495 495	0	495
1	C007	495	Total C 495 495	0	495
1	A008	495	Total C 495 495	0	495
1	B008	495	Total C 495 495	0	495
1	C008	495	Total C 495 495	0	495
1	B000	495	Total C 495 495	0	495
1	A009	495	Total C 495 495	0	495
1	B009	495	Total C 495 495	0	495

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
1	C009	495	Total C 495 495	0	495
1	A010	495	Total C 495 495	0	495
1	B010	495	Total C 495 495	0	495
1	C010	495	Total C 495 495	0	495
1	A011	495	Total C 495 495	0	495
1	B011	495	Total C 495 495	0	495
1	C011	495	Total C 495 495	0	495
1	A012	495	Total C 495 495	0	495
1	B012	495	Total C 495 495	0	495
1	C012	495	Total C 495 495	0	495
1	C000	495	Total C 495 495	0	495
1	A013	495	Total C 495 495	0	495
1	B013	495	Total C 495 495	0	495
1	C013	495	Total C 495 495	0	495
1	A014	495	Total C 495 495	0	495
1	B014	495	Total C 495 495	0	495
1	C014	495	Total C 495 495	0	495
1	A015	495	Total C 495 495	0	495
1	B015	495	Total C 495 495	0	495
1	C015	495	Total C 495 495	0	495
1	A016	495	Total C 495 495	0	495

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
1	B016	495	Total C 495 495	0	495
1	C016	495	Total C 495 495	0	495
1	A017	495	Total C 495 495	0	495
1	B017	495	Total C 495 495	0	495
1	C017	495	Total C 495 495	0	495
1	A018	495	Total C 495 495	0	495
1	B018	495	Total C 495 495	0	495
1	C018	495	Total C 495 495	0	495
1	A019	495	Total C 495 495	0	495
1	B019	495	Total C 495 495	0	495
1	C019	495	Total C 495 495	0	495
1	A020	495	Total C 495 495	0	495
1	B020	495	Total C 495 495	0	495
1	C020	495	Total C 495 495	0	495
1	A021	495	Total C 495 495	0	495
1	B021	495	Total C 495 495	0	495
1	C021	495	Total C 495 495	0	495
1	A022	495	Total C 495 495	0	495
1	B022	495	Total C 495 495	0	495
1	C022	495	Total C 495 495	0	495
1	A023	495	Total C 495 495	0	495

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
1	B023	495	Total C 495 495	0	495
1	C023	495	Total C 495 495	0	495
1	A001	495	Total C 495 495	0	495
1	B001	495	Total C 495 495	0	495
1	C001	495	Total C 495 495	0	495
1	A002	495	Total C 495 495	0	495
1	B002	495	Total C 495 495	0	495
1	C002	495	Total C 495 495	0	495
1	A003	495	Total C 495 495	0	495
1	B003	495	Total C 495 495	0	495
1	C003	495	Total C 495 495	0	495
1	A004	495	Total C 495 495	0	495
1	B004	495	Total C 495 495	0	495

- Molecule 2 is a protein called Protein prM.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D004	166	Total C 166 166	0	166
2	E004	166	Total C 166 166	0	166
2	F004	166	Total C 166 166	0	166
2	D005	166	Total C 166 166	0	166
2	E005	166	Total C 166 166	0	166
2	F005	166	Total C 166 166	0	166

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D006	166	Total C 166 166	0	166
2	E006	166	Total C 166 166	0	166
2	F006	166	Total C 166 166	0	166
2	D007	166	Total C 166 166	0	166
2	E007	166	Total C 166 166	0	166
2	F007	166	Total C 166 166	0	166
2	D008	166	Total C 166 166	0	166
2	E008	166	Total C 166 166	0	166
2	F008	166	Total C 166 166	0	166
2	D009	166	Total C 166 166	0	166
2	E009	166	Total C 166 166	0	166
2	F009	166	Total C 166 166	0	166
2	D010	166	Total C 166 166	0	166
2	E010	166	Total C 166 166	0	166
2	F010	166	Total C 166 166	0	166
2	D011	166	Total C 166 166	0	166
2	E011	166	Total C 166 166	0	166
2	F011	166	Total C 166 166	0	166
2	D012	166	Total C 166 166	0	166
2	E012	166	Total C 166 166	0	166
2	F012	166	Total C 166 166	0	166

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D013	166	Total C 166 166	0	166
2	E013	166	Total C 166 166	0	166
2	F013	166	Total C 166 166	0	166
2	D014	166	Total C 166 166	0	166
2	E014	166	Total C 166 166	0	166
2	F014	166	Total C 166 166	0	166
2	D015	166	Total C 166 166	0	166
2	E015	166	Total C 166 166	0	166
2	F015	166	Total C 166 166	0	166
2	D016	166	Total C 166 166	0	166
2	E016	166	Total C 166 166	0	166
2	F016	166	Total C 166 166	0	166
2	D000	166	Total C 166 166	0	166
2	D017	166	Total C 166 166	0	166
2	E017	166	Total C 166 166	0	166
2	F017	166	Total C 166 166	0	166
2	D018	166	Total C 166 166	0	166
2	E018	166	Total C 166 166	0	166
2	F018	166	Total C 166 166	0	166
2	D019	166	Total C 166 166	0	166
2	E019	166	Total C 166 166	0	166

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf	Trace
2	F019	166	Total C 166 166	0	166
2	D020	166	Total C 166 166	0	166
2	E020	166	Total C 166 166	0	166
2	F020	166	Total C 166 166	0	166
2	D021	166	Total C 166 166	0	166
2	E000	166	Total C 166 166	0	166
2	E021	166	Total C 166 166	0	166
2	F021	166	Total C 166 166	0	166
2	D022	166	Total C 166 166	0	166
2	E022	166	Total C 166 166	0	166
2	F022	166	Total C 166 166	0	166
2	D023	166	Total C 166 166	0	166
2	E023	166	Total C 166 166	0	166
2	F023	166	Total C 166 166	0	166
2	F000	166	Total C 166 166	0	166
2	D001	166	Total C 166 166	0	166
2	E001	166	Total C 166 166	0	166
2	F001	166	Total C 166 166	0	166
2	D002	166	Total C 166 166	0	166
2	E002	166	Total C 166 166	0	166
2	F002	166	Total C 166 166	0	166

Continued on next page...

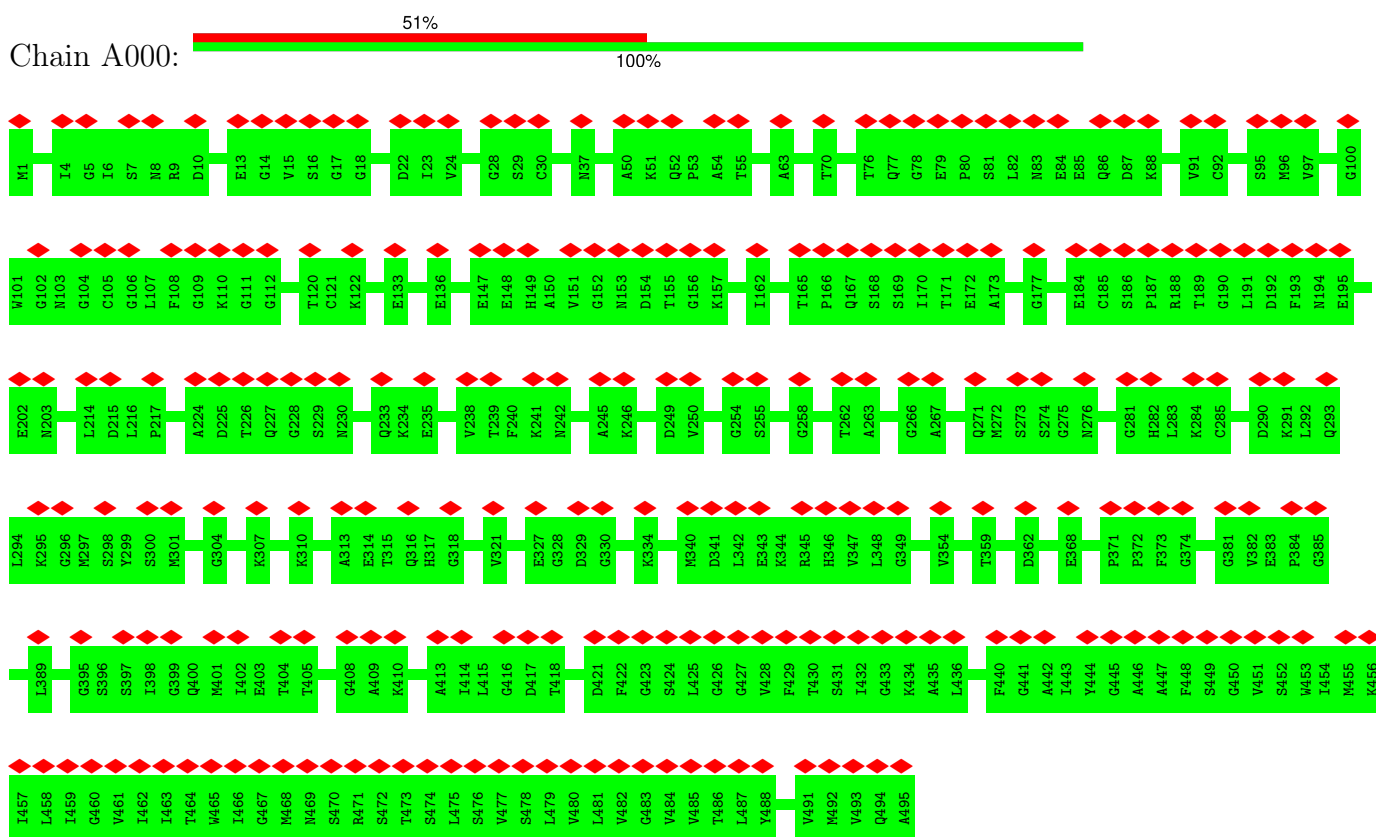
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf	Trace
2	D003	166	Total 166	C 166	0	166
2	E003	166	Total 166	C 166	0	166
2	F003	166	Total 166	C 166	0	166

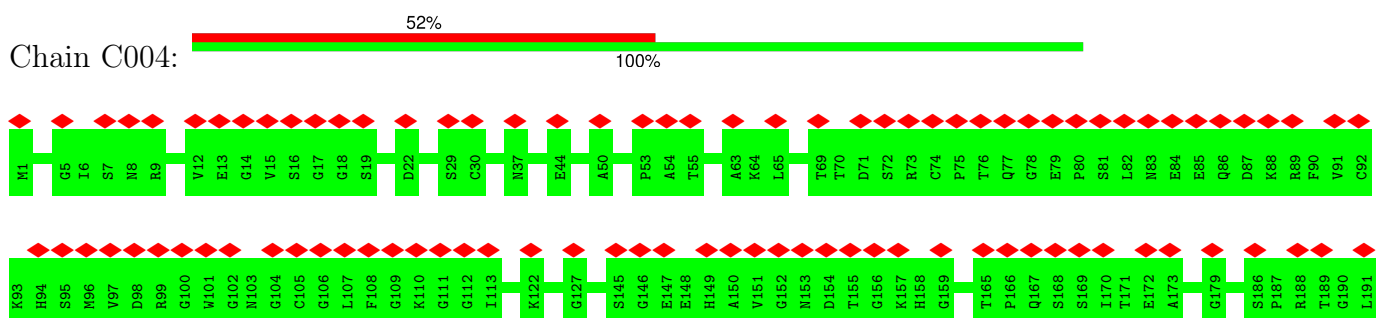
3 Residue-property plots

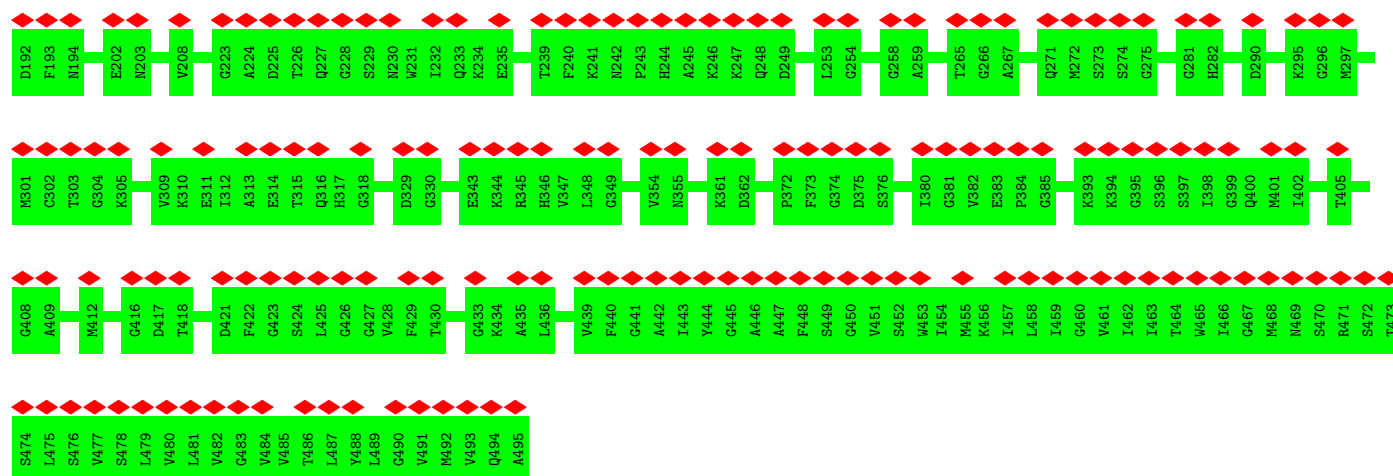
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: glycoprotein E

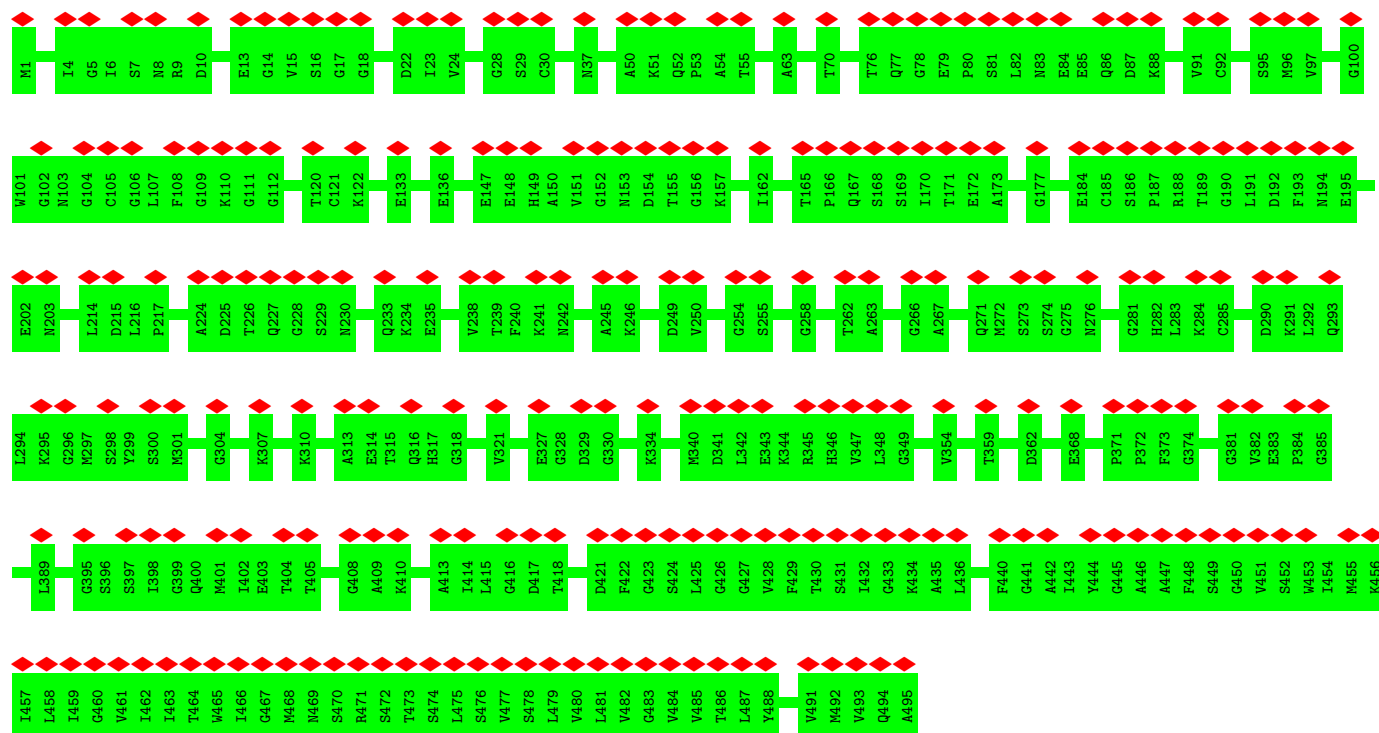


- Molecule 1: glycoprotein E

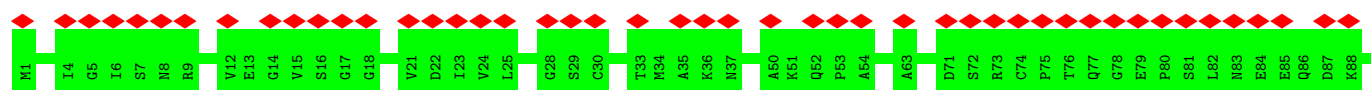


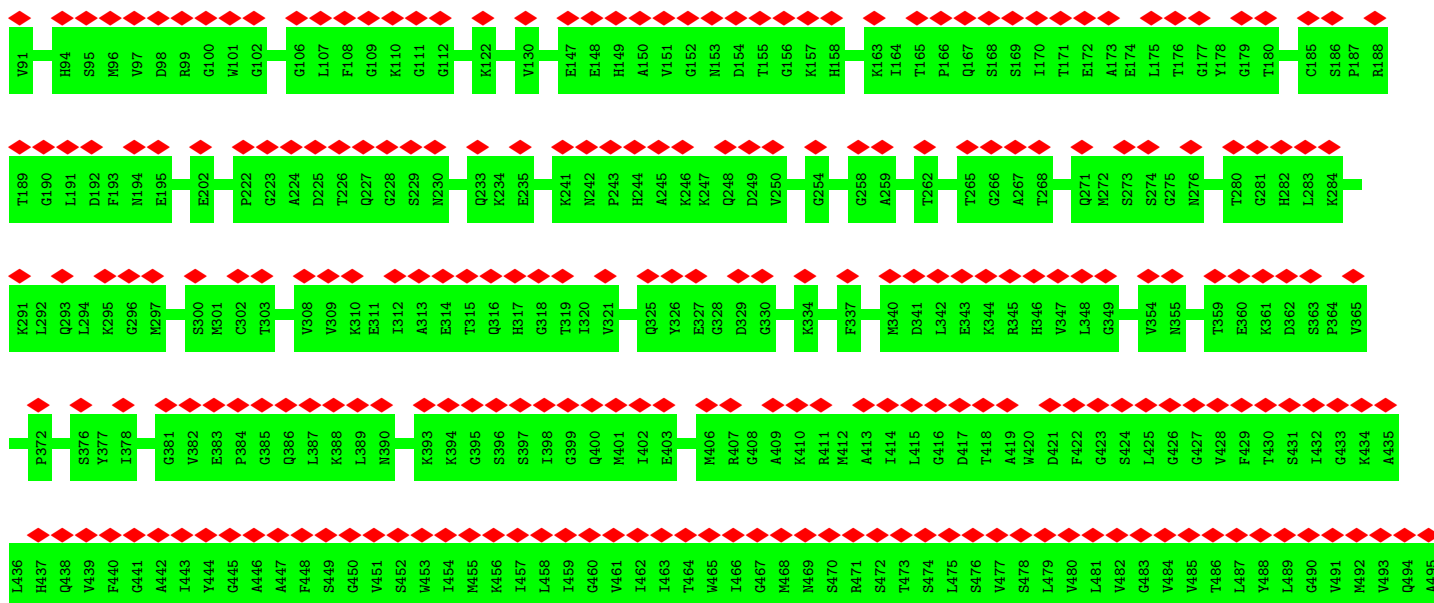


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



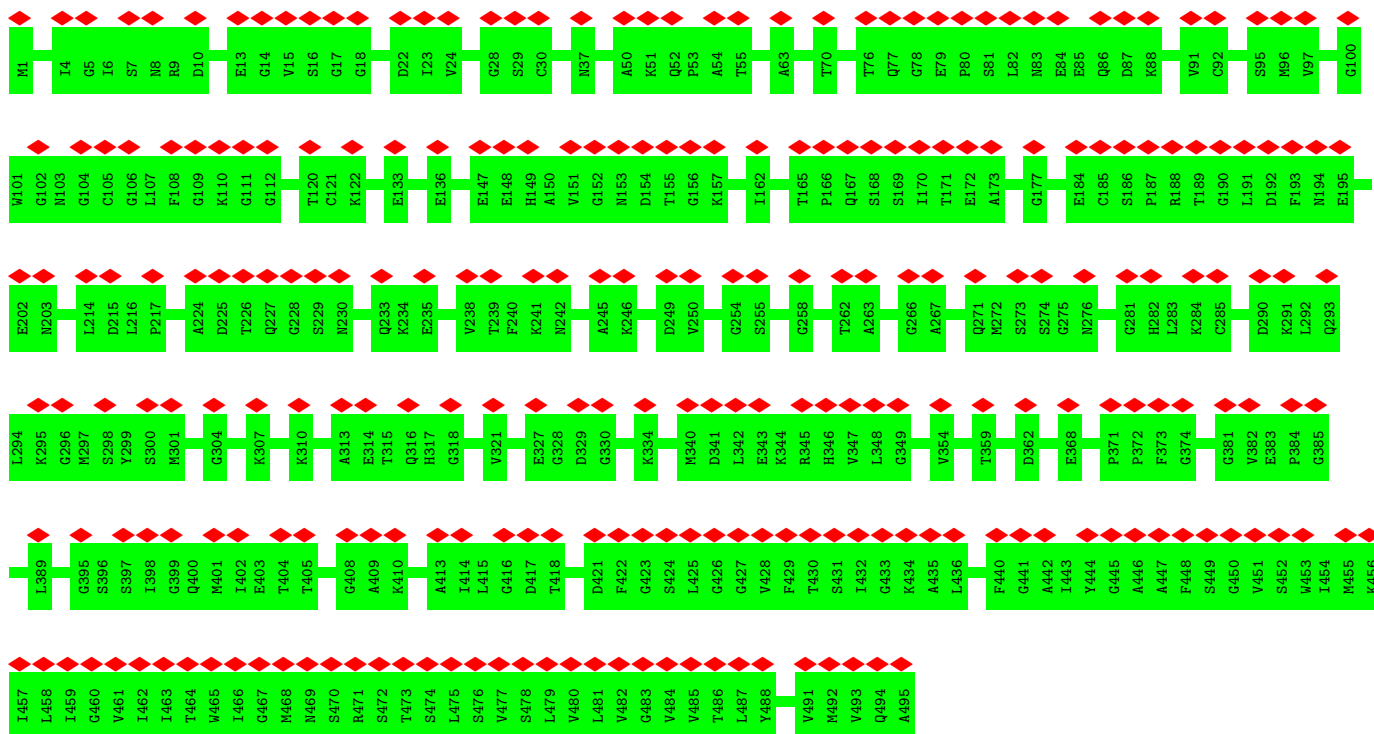


• Molecule 1: glycoprotein E

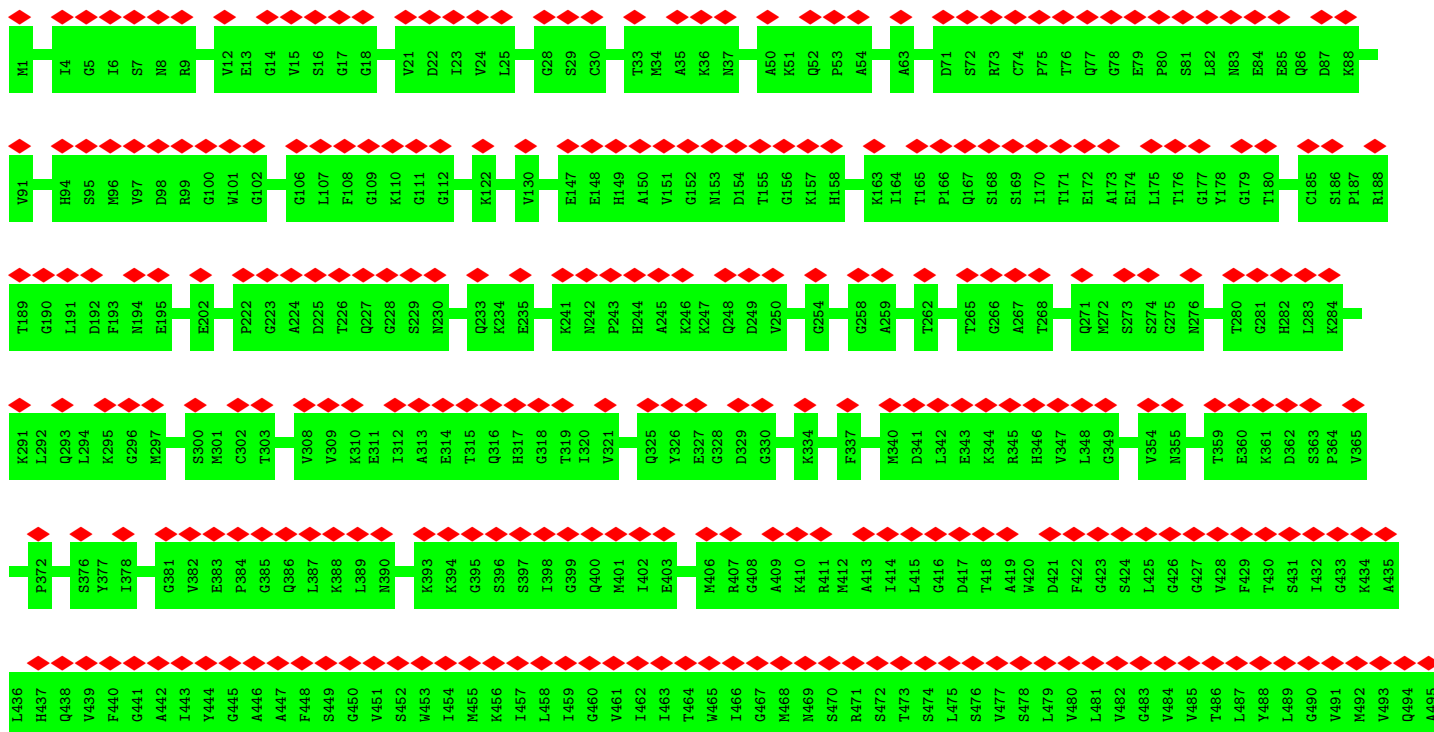


• Molecule 1: glycoprotein E





• Molecule 1: glycoprotein E



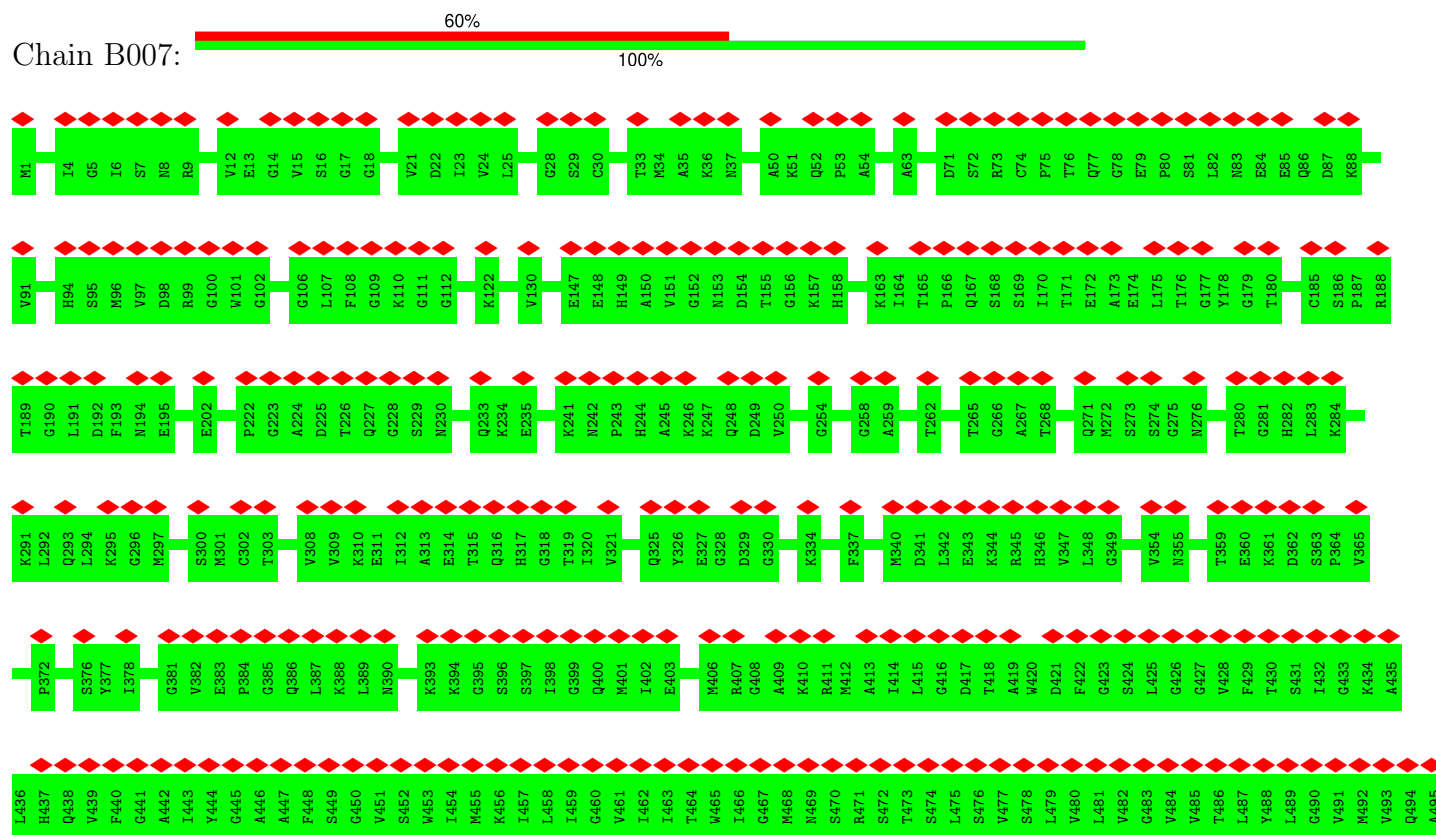
• Molecule 1: glycoprotein E

S474	G408	M301	D192	K93	M1
L475	A409	C302	F193	H94	G5
S476		T303	H194	S95	I6
V477	M412	G304		M96	S7
S478	G416	K305	E202	D98	N8
L479	D417		M203	R99	R9
V480	T418	V309		G100	
L481		K310	V206	W101	V12
V482		E311		G102	E13
G483	D421	T312	G223	N103	G14
V484	F422	A313	A224	G104	V15
T485	G423	E314	D225	C105	S16
V486	S424	T315	T226	G106	G17
L487	L425	Q316	Q227	L107	G18
V488	G426	H317	G228	F108	S19
L489	G427	G318	S229	G109	D22
G490	V428	D329	W230	K110	
V491	F429	G330	W231	G111	S29
L492	T430		T232	G112	C30
V493		E343	Q233	I113	
G494	G433	K344	K234		N37
A495	K434	R345	F235	K122	E44
	A435	H346	T239	G127	
	L436	V347	F240		A50
		L348	K241	S145	P63
	V439	F440	N242	G146	A54
G441	G441		P243	E147	T55
A442	A442	V354	H244	E148	
I443	I443	M355	A245	H149	
V444	Y444		K246	A150	A63
G445	G445	K361	K247	V151	K64
A446	A446	D362	Q248	G152	L65
A447	A447		D249	N153	
F448	F448	P372	L253	D154	T69
S449	S449	G373	G254	T155	D71
G450	G450	C374		G156	S72
V451	V451	D375	G258	K157	R73
S452	S452	S376	A259	H158	C74
W453	W453			G159	P75
L454	L454	G381	T265	T165	T76
M455	M455	V382	G266	P166	Q77
K456	K456	E383	A267	Q167	G78
L457	L457	P384		S168	E79
L458	L458	G385	Q271	S169	P80
I459	I459		M272	I170	S81
G460	G460	K393	S273	T171	L82
V461	V461	K394	G274	E172	N83
L462	L462	G395	G275	A173	E84
I463	I463	S396		G179	E85
T464	T464	S397	G281		Q86
V465	V465	I398	H282		D87
L466	L466	G399	D290	S186	K88
G467	G467	Q400		P187	R89
M468	M468	N401	K295	R188	F90
M469	M469	L402	G296	T189	G90
S470	S470		M297	L191	V91
R471	R471	T405			C92
T472	T472				

I457	L389	L294	E202	W101	M1
L458	G395	G295	W203	G102	I4
I459	S396	G296	L214	N103	G5
G460	S397	M297	D215	G104	I6
V461	I398	Y299	P217	G105	S7
I462	I399	S300	P217	G106	N8
I463	G399	M301	E224	F108	R9
T464	Q400	G304	D225	G109	D10
V465	M401	G304	D225	G110	E13
I466	I402	K307	T226	G111	G14
G467	E403	K310	Q227	G112	V15
M468	T404	K310	S228	T120	S16
M469	T405	A313	G229	C121	G17
S470	Q408	E314	W230	K122	G18
R471	A409	T315	Q233	E133	D22
S472	K410	Q316	Y234	E136	I23
T473	A413	H317	E235	E147	V24
S474	I414	G318	V236	E148	G28
L475	L415	V321	T239	H149	S29
S476	G416	E327	K241	A150	C30
V477	D417	G328	W242	V151	N37
S478	T418	D329	A245	G152	I50
L479	D421	G330	K246	N153	A50
V480	F422	K334	D249	D154	K51
L481	G423	M340	V250	T155	Q52
S482	S424	D341	G254	G156	P53
G483	L425	L342	S255	K157	A54
V484	G426	E343	G258	T162	T55
S485	G427	R344	T262	T165	A63
L486	G427	R345	A263	P166	T70
V487	V429	H346	G266	Q167	T76
Y488	S431	V347	A267	S168	Q77
V489	I432	L348	Q271	I170	G78
M492	G433	G349	T272	T171	E79
V493	K434	V354	E273	E172	P80
G494	A435	T359	S273	A173	S81
A495	L436	D362	G275	G177	L82
		E368	W276	E184	N83
		F371	G281	C185	E84
		P372	H282	S186	Q86
		F373	L283	T187	D87
		G374	K284	R188	K98
		G381	C285	T189	V91
		V382	D290	G190	C92
		E383	L291	L191	S95
		P384	L292	D192	N96
		G385	Q293	F193	V97
				N194	G100
				E195	

• Molecule 1: glycoprotein E

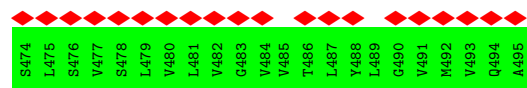
Chain B007:



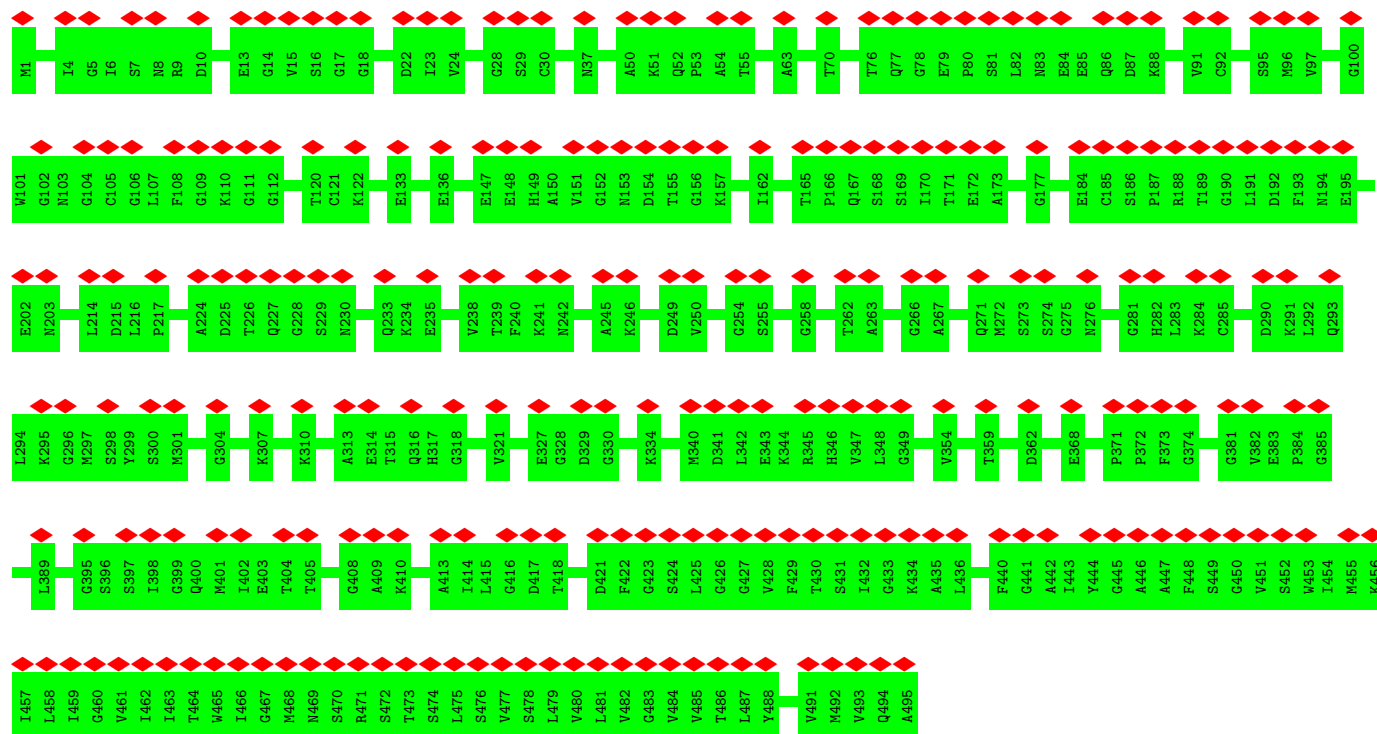
• Molecule 1: glycoprotein E

Chain C007:

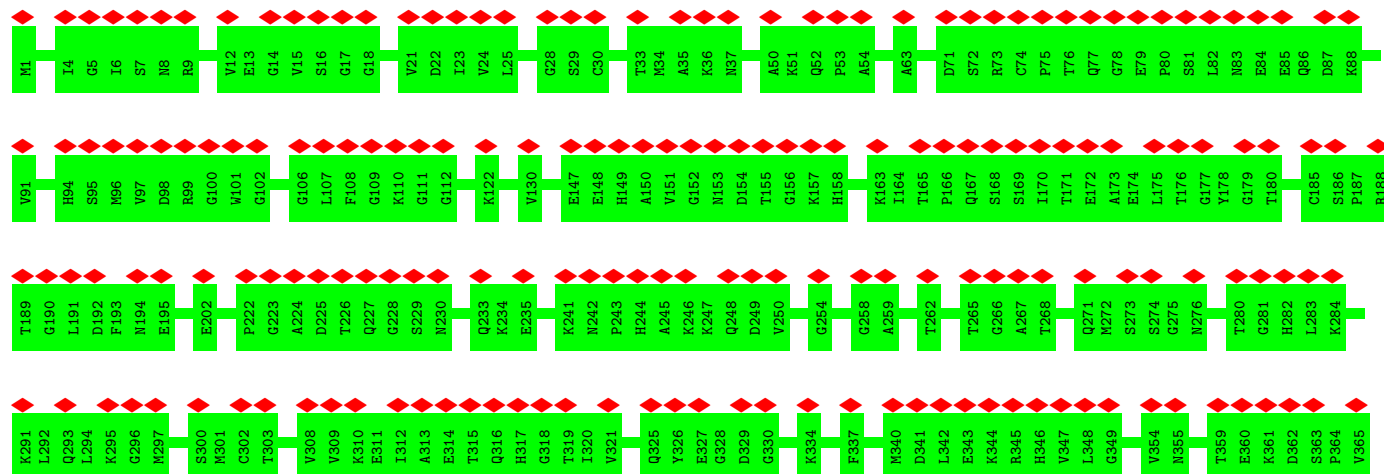


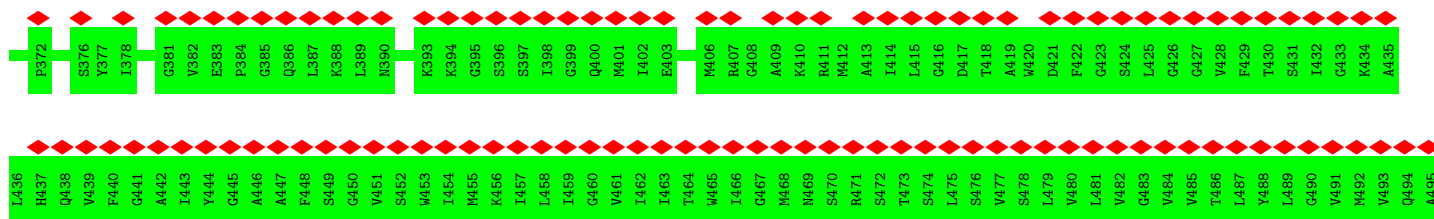


• Molecule 1: glycoprotein E

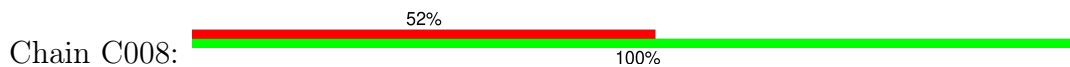


• Molecule 1: glycoprotein E

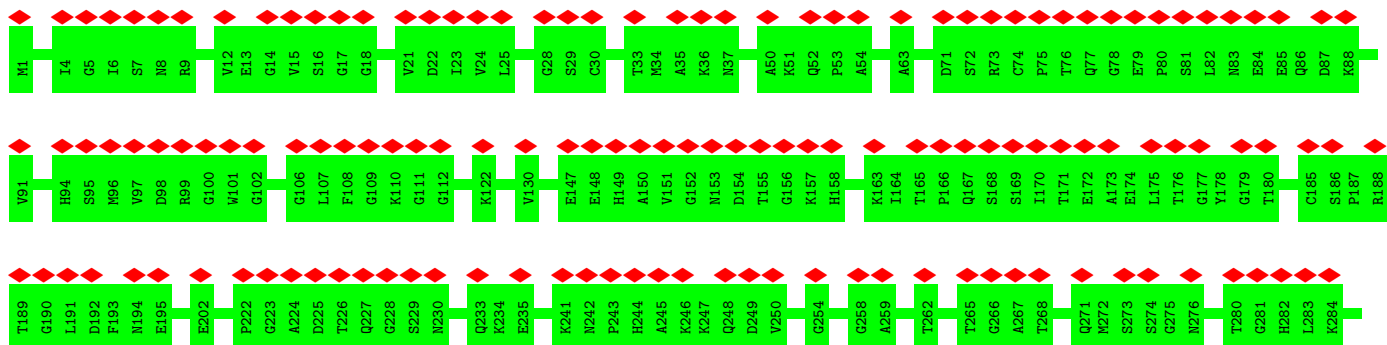


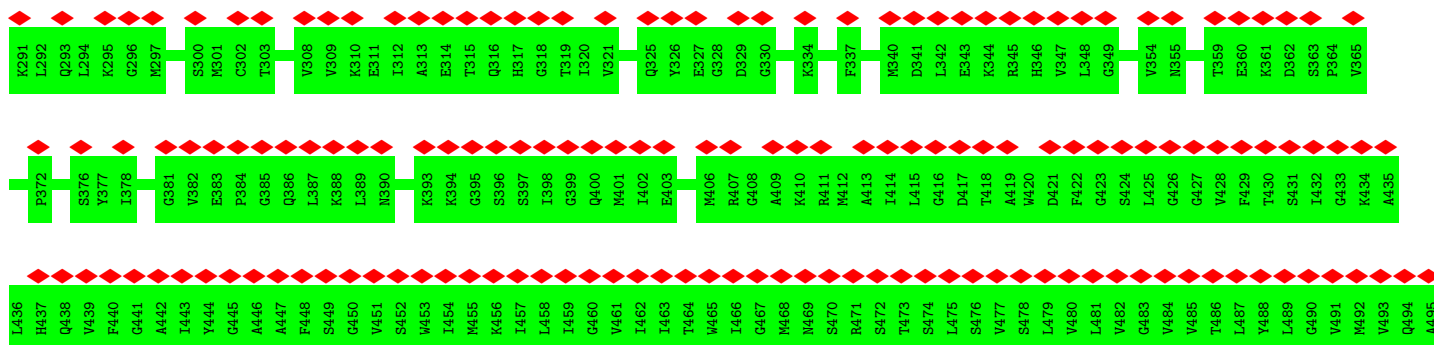


• Molecule 1: glycoprotein E

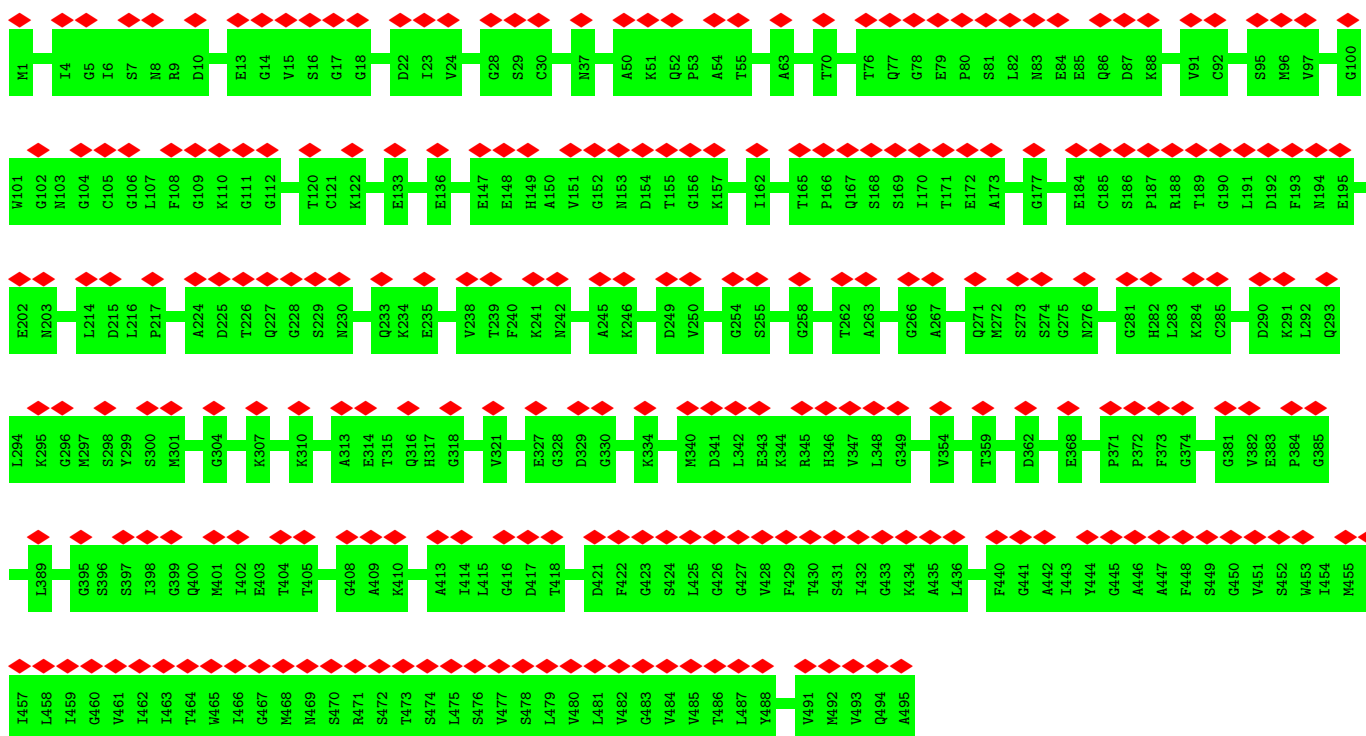


• Molecule 1: glycoprotein E

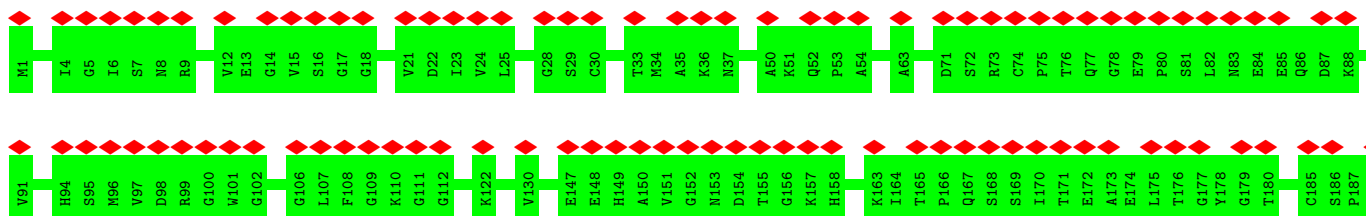


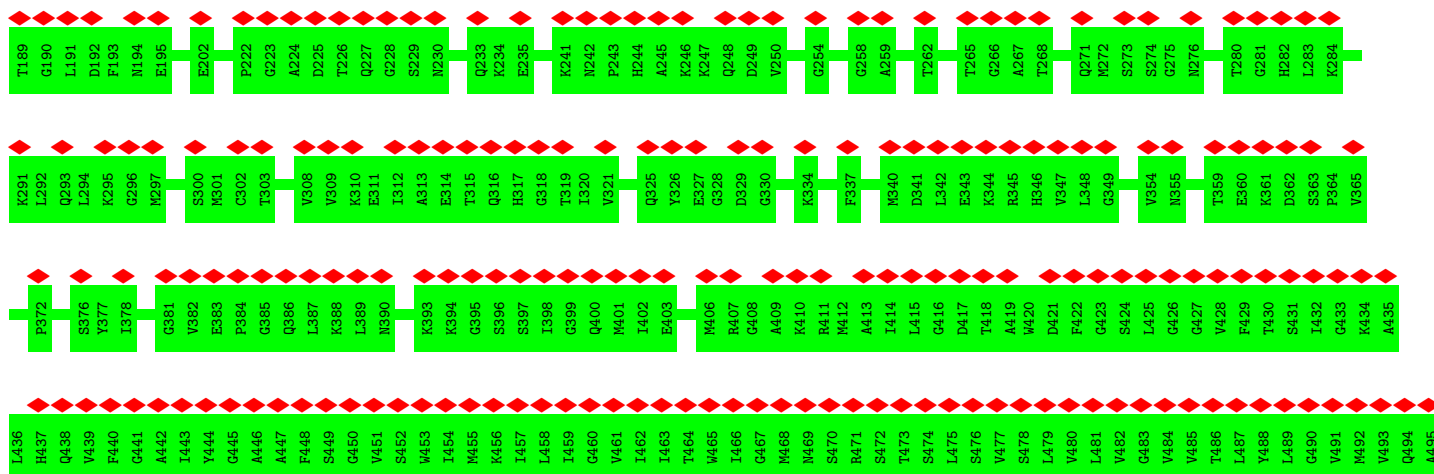


- Molecule 1: glycoprotein E



- Molecule 1: glycoprotein E

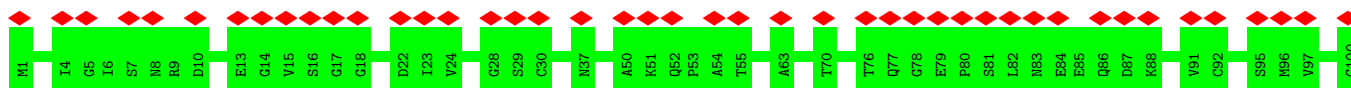


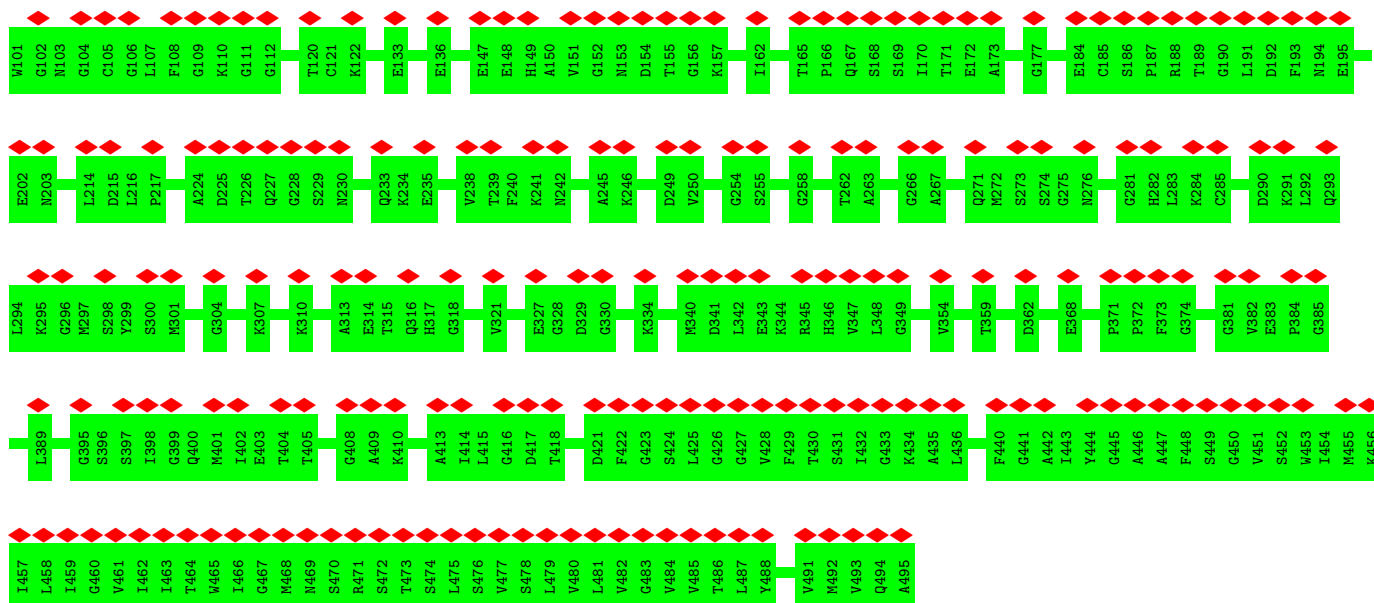


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E





• Molecule 1: glycoprotein E

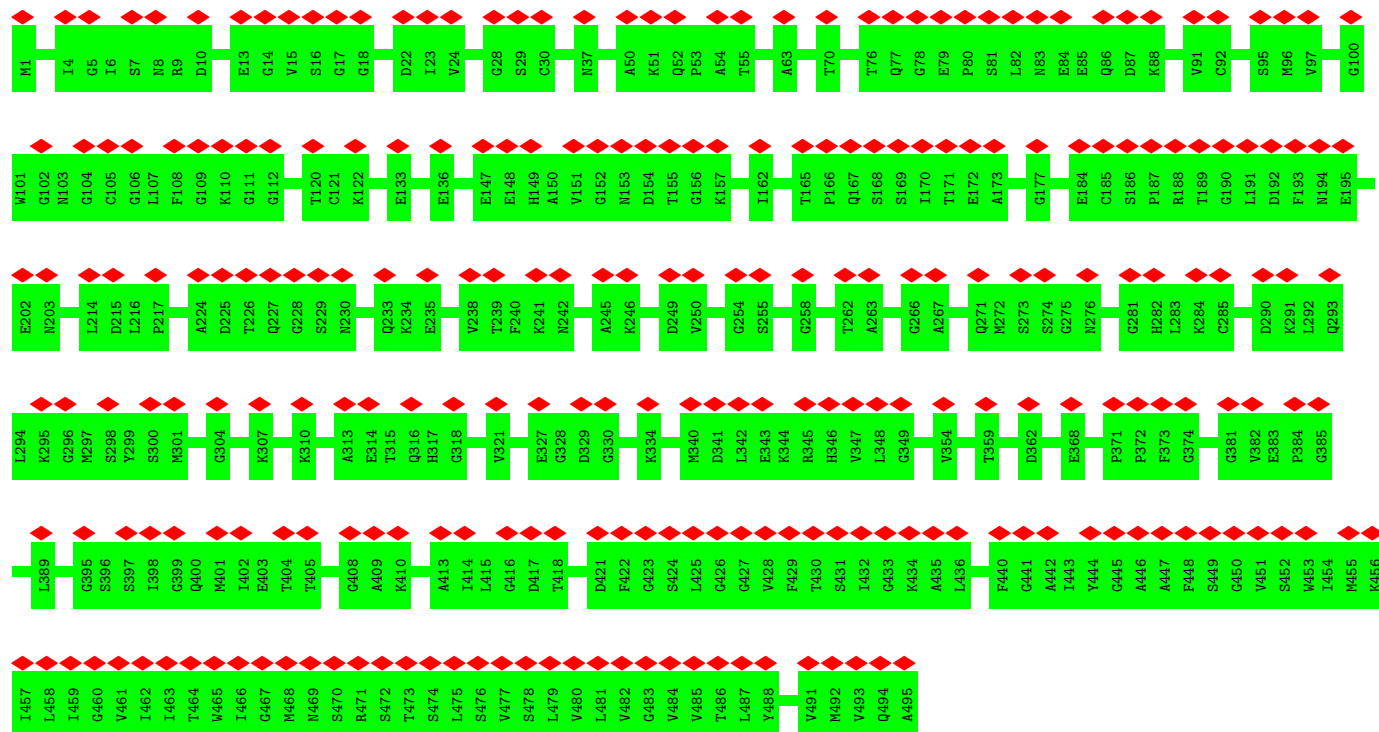


• Molecule 1: glycoprotein E





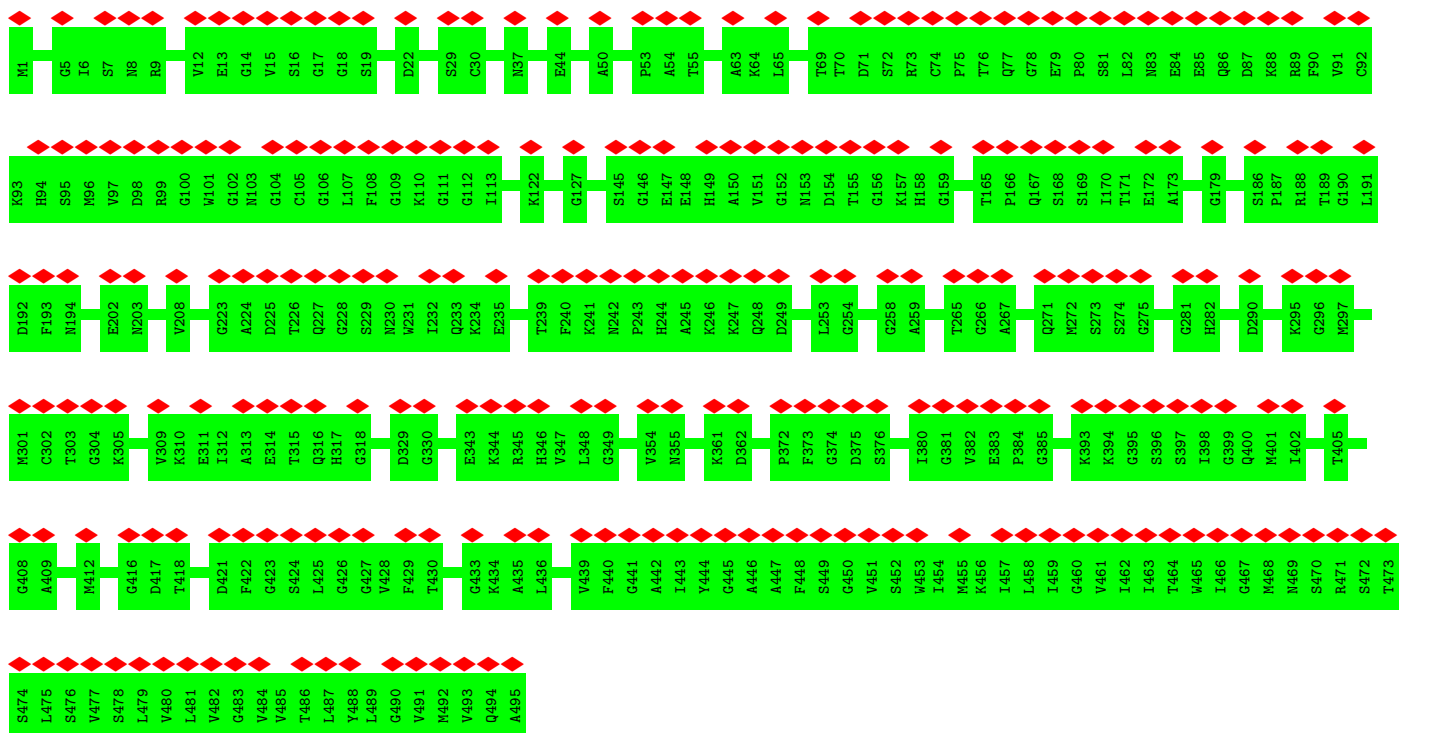
• Molecule 1: glycoprotein E



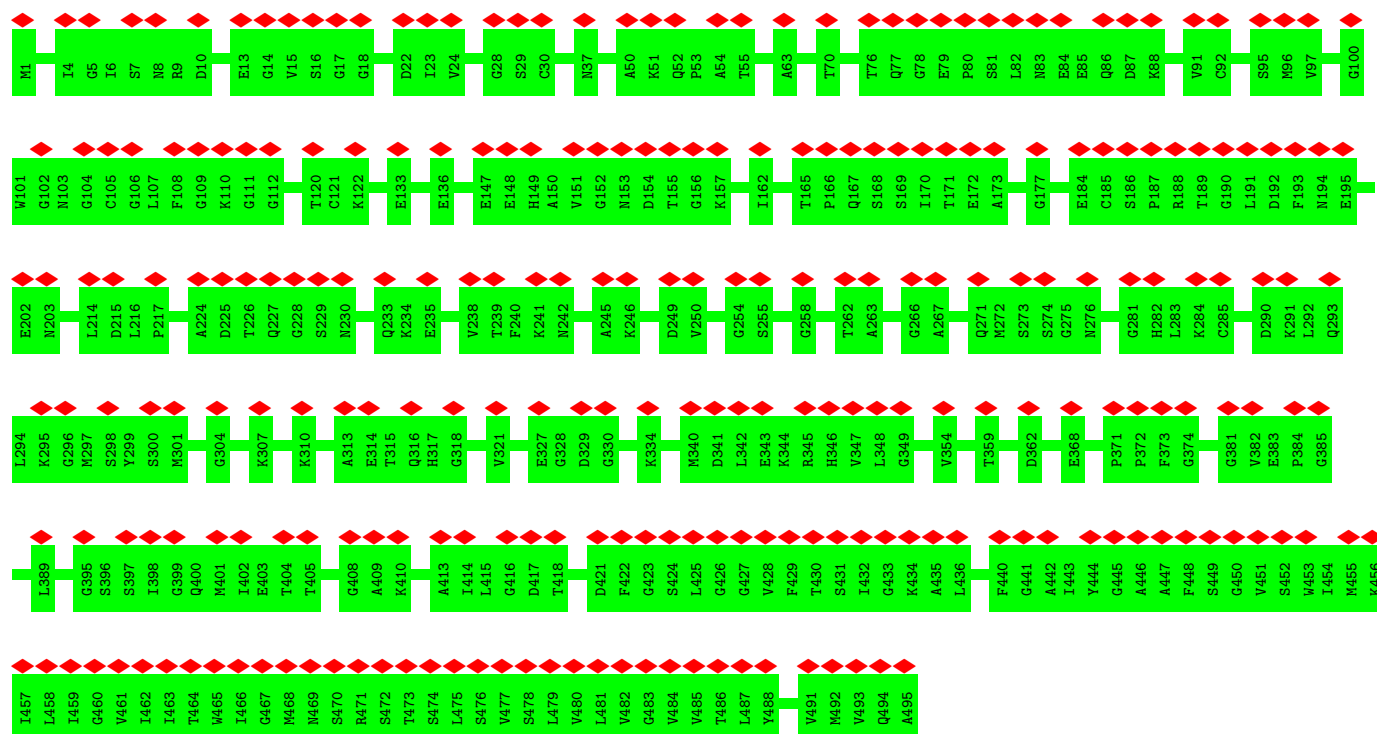
• Molecule 1: glycoprotein E



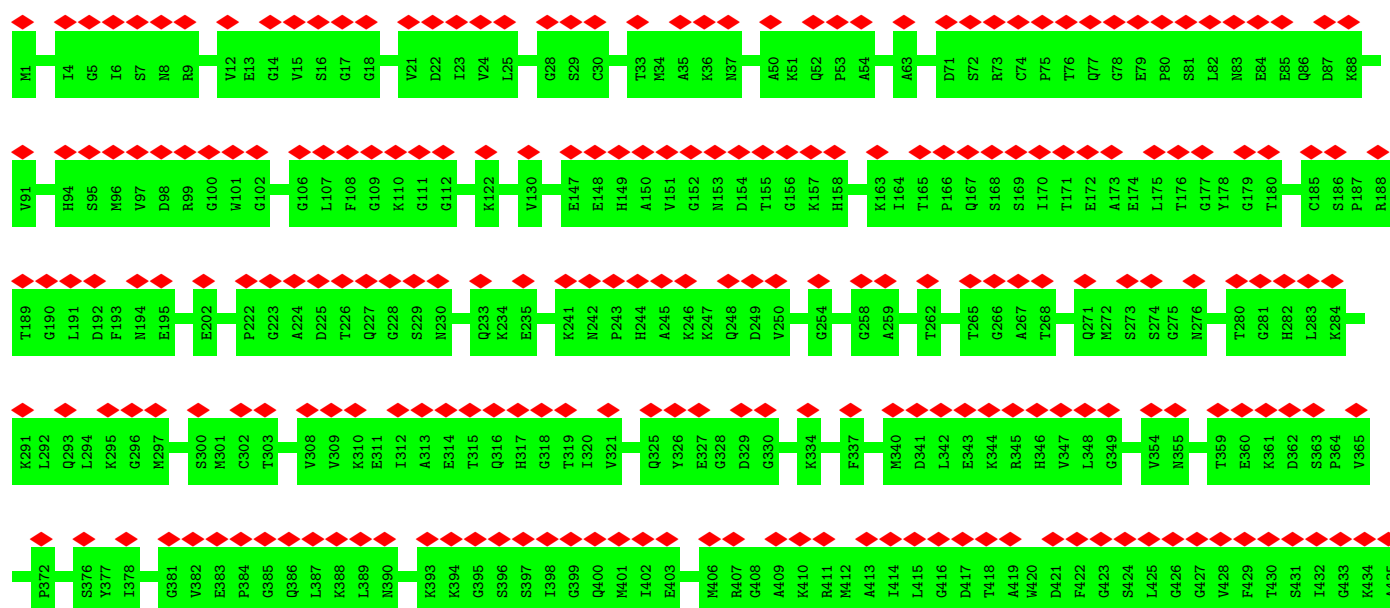
• Molecule 1: glycoprotein E

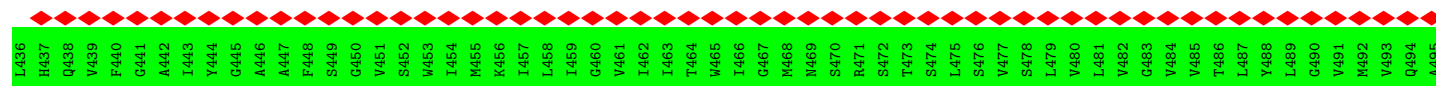


- Molecule 1: glycoprotein E

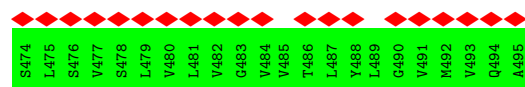
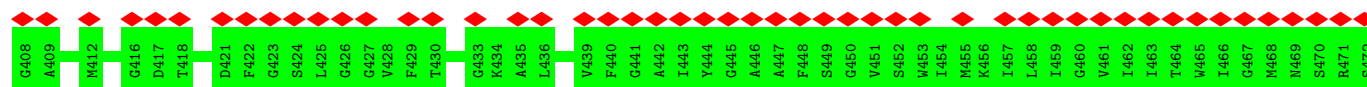
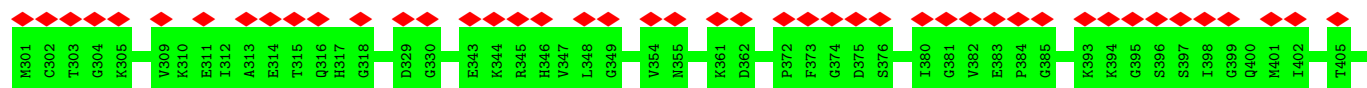
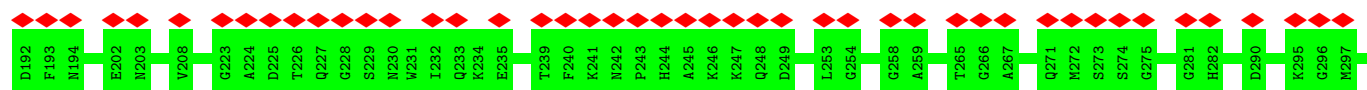
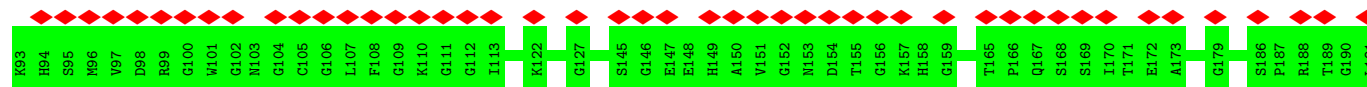
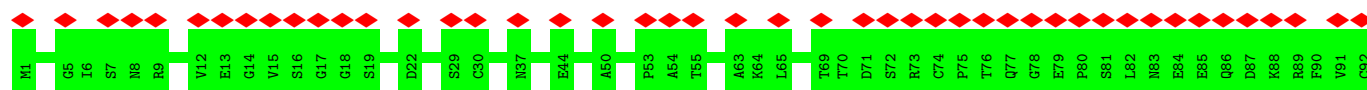


- Molecule 1: glycoprotein E

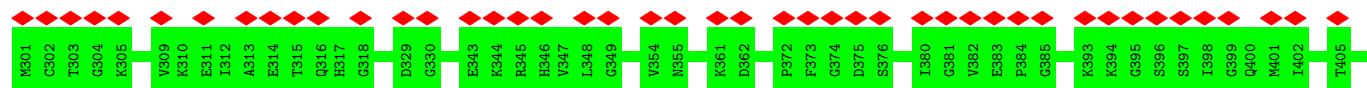
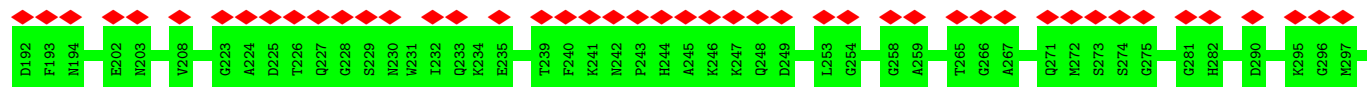
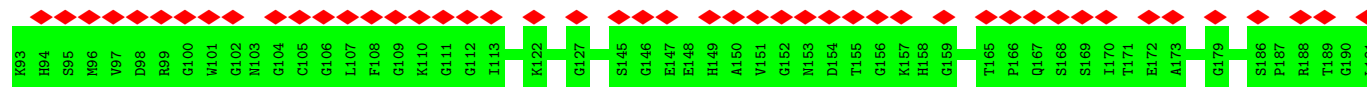
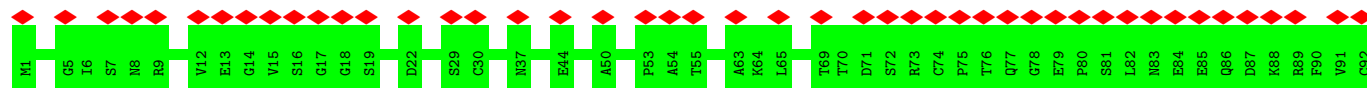


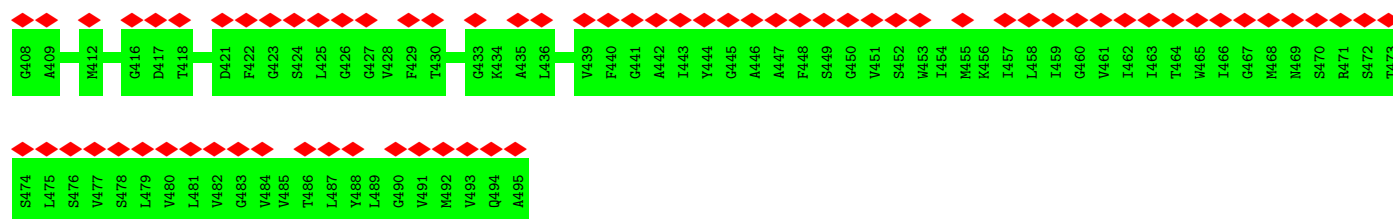


• Molecule 1: glycoprotein E

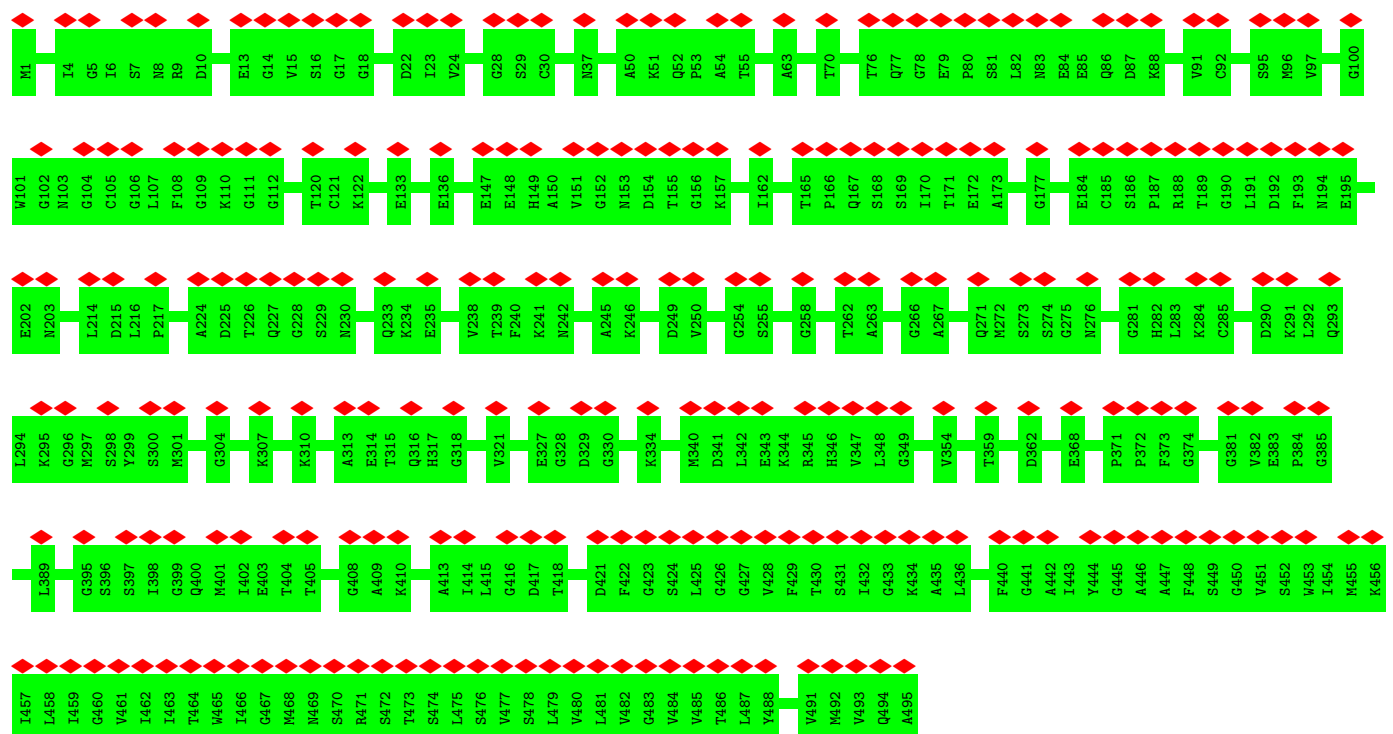


• Molecule 1: glycoprotein E

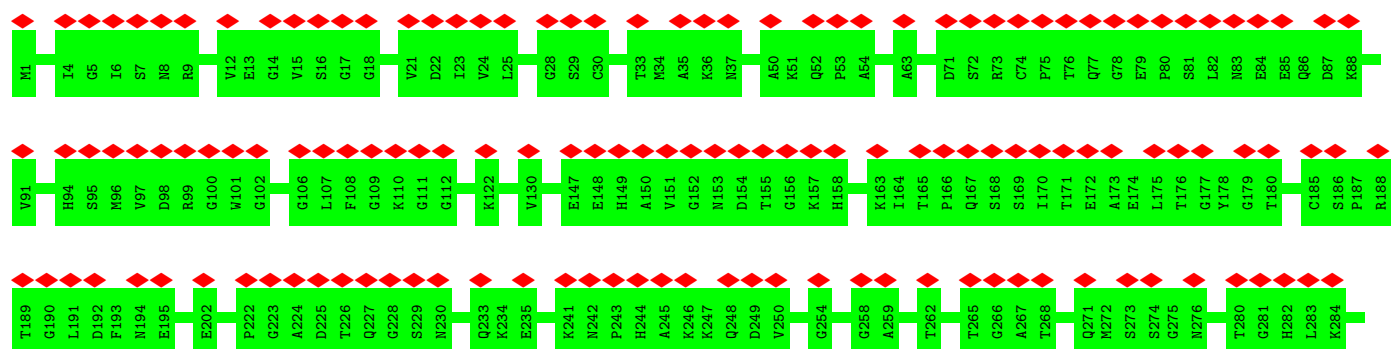


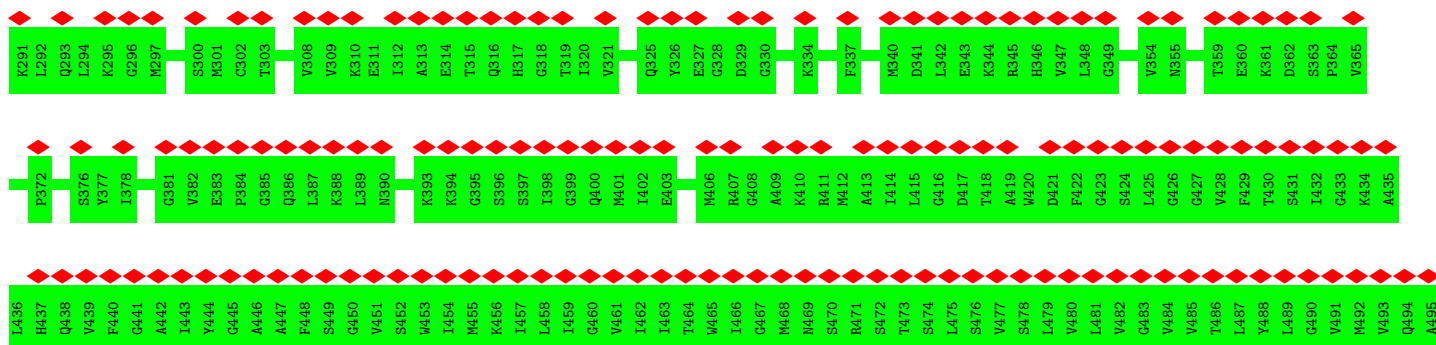


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

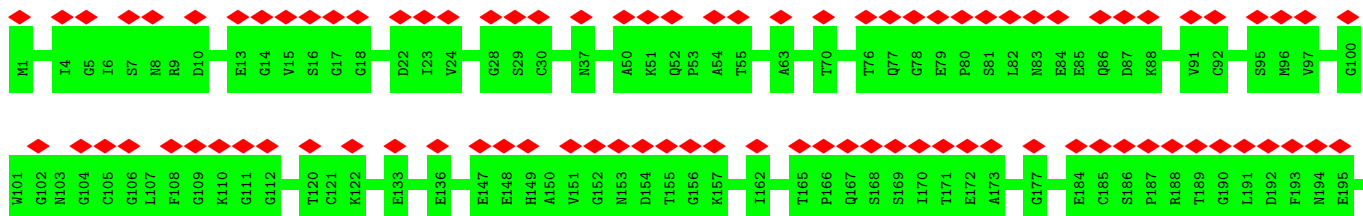


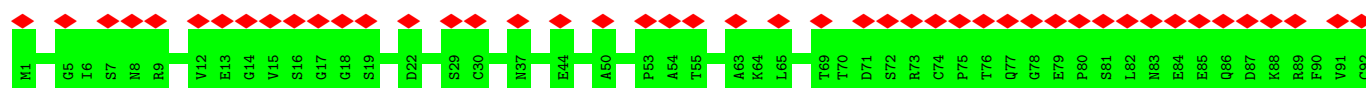


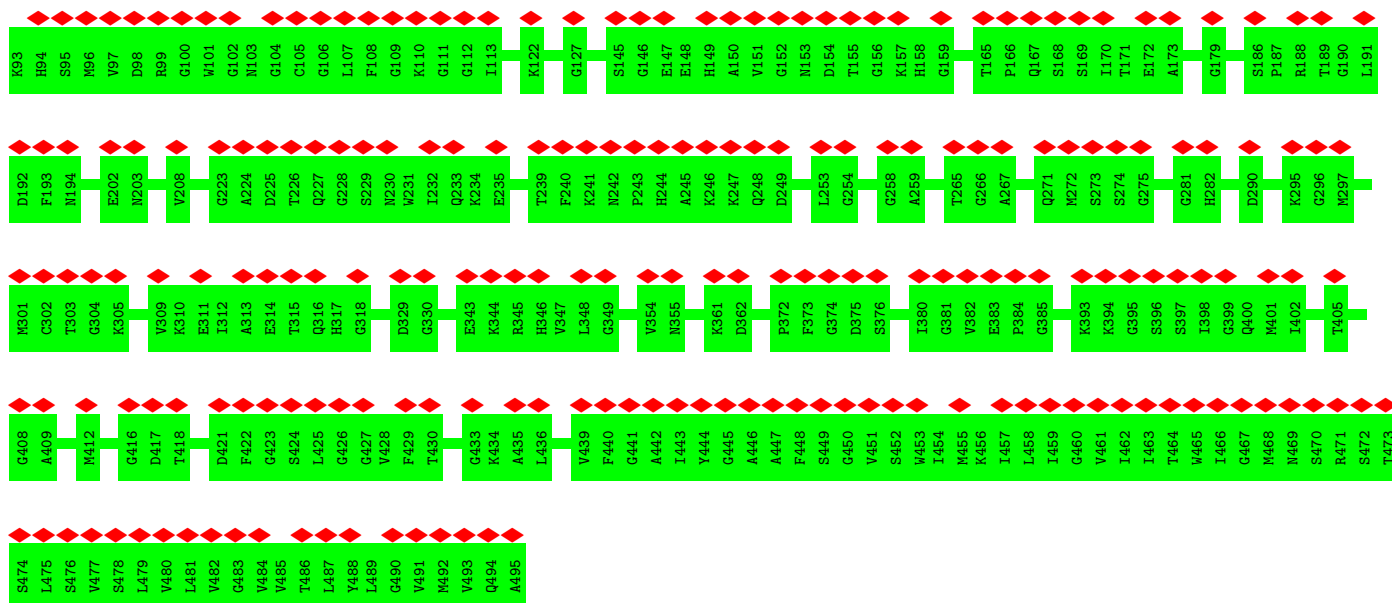
• Molecule 1: glycoprotein E



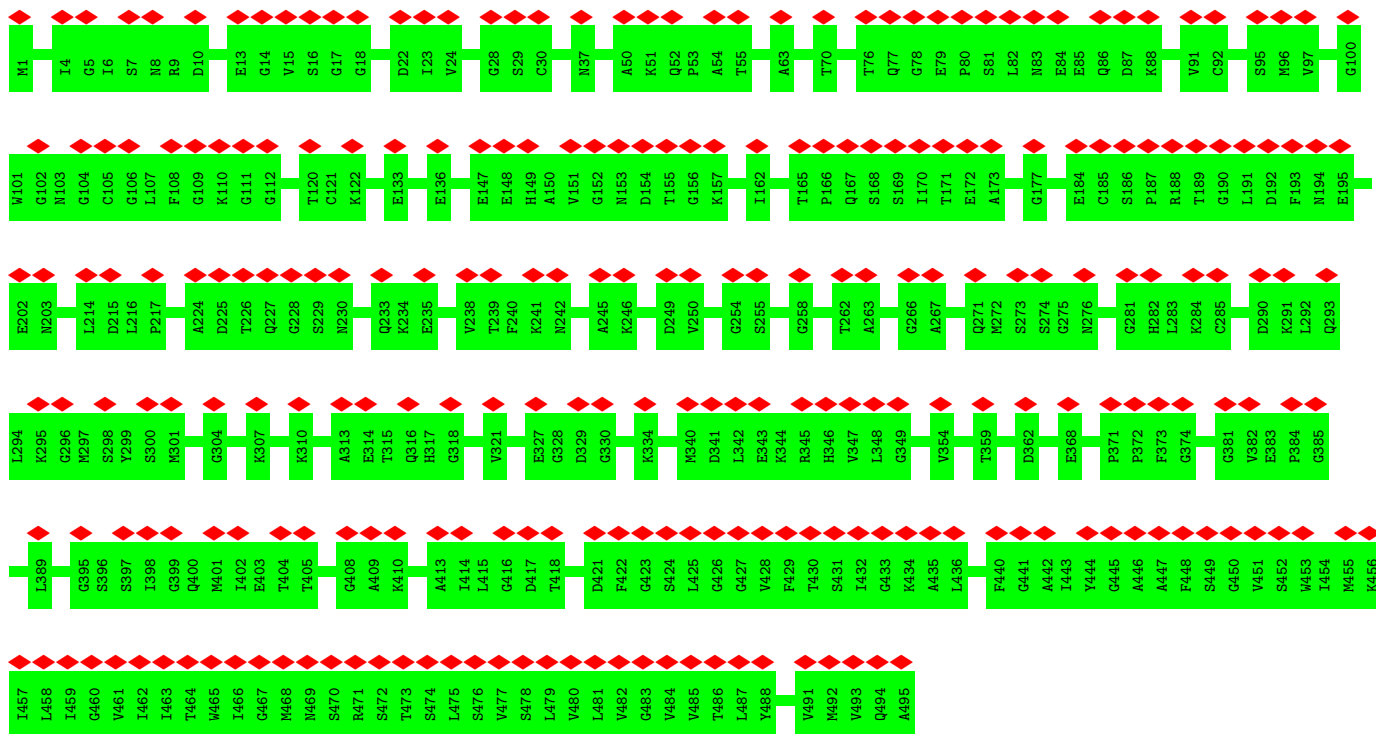
• Molecule 1: glycoprotein E







• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

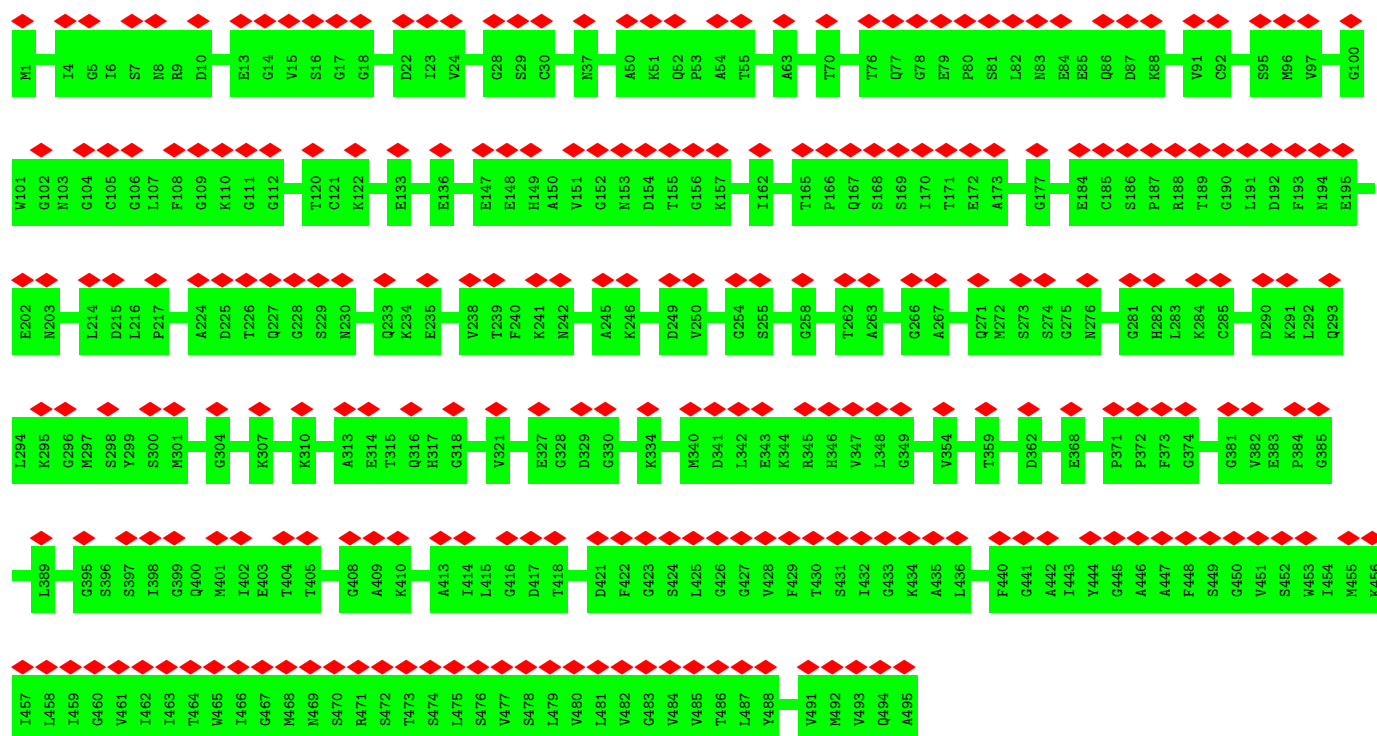




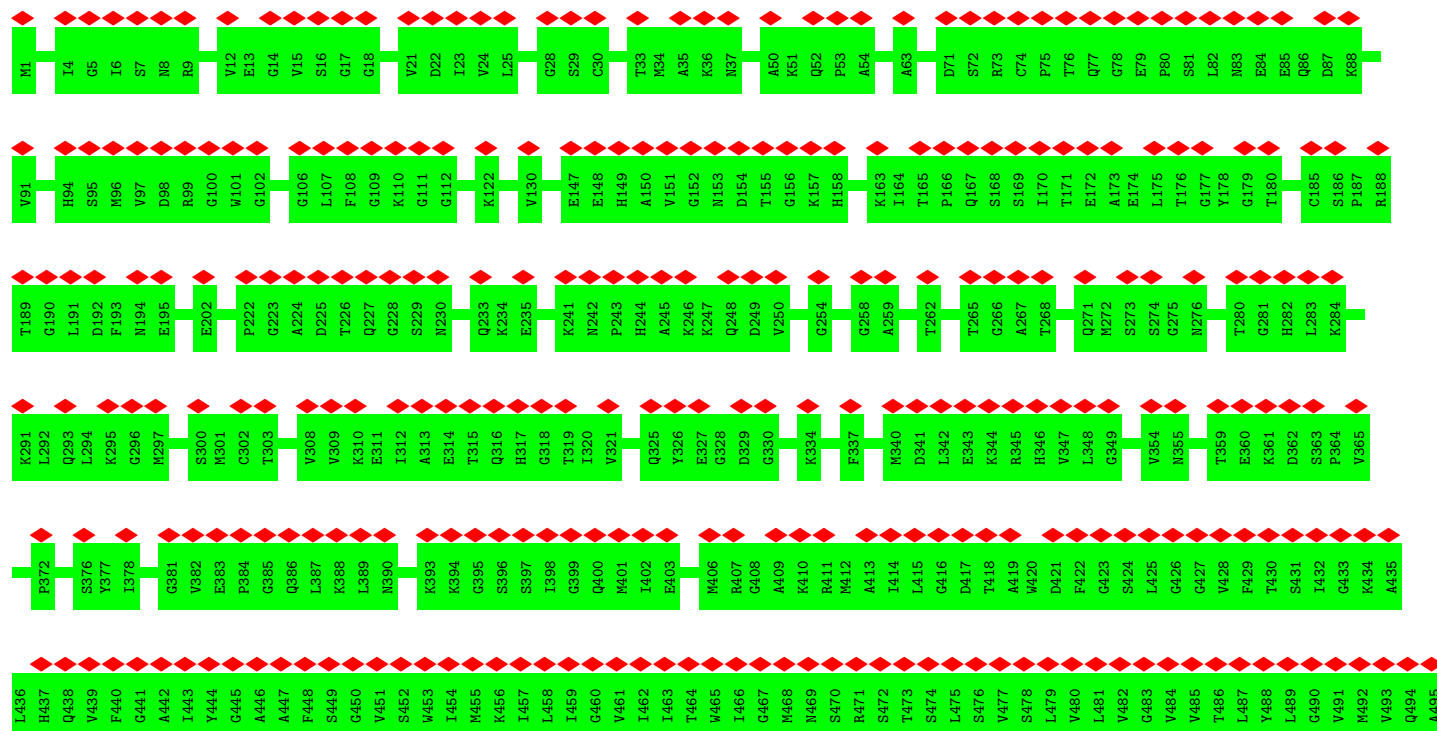
- Molecule 1: glycoprotein E



- Molecule 1: glycoprotein E

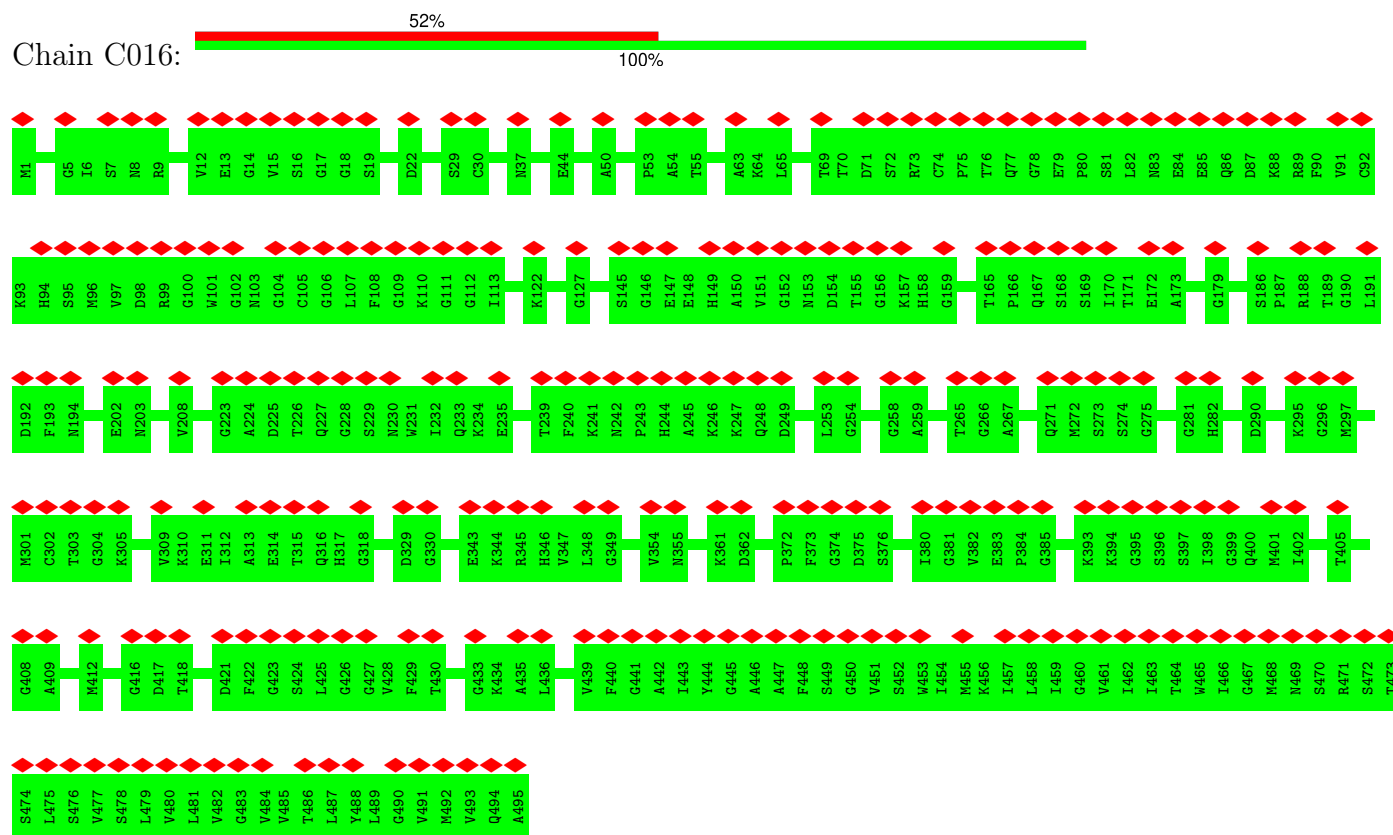


• Molecule 1: glycoprotein E



- Molecule 1: glycoprotein E

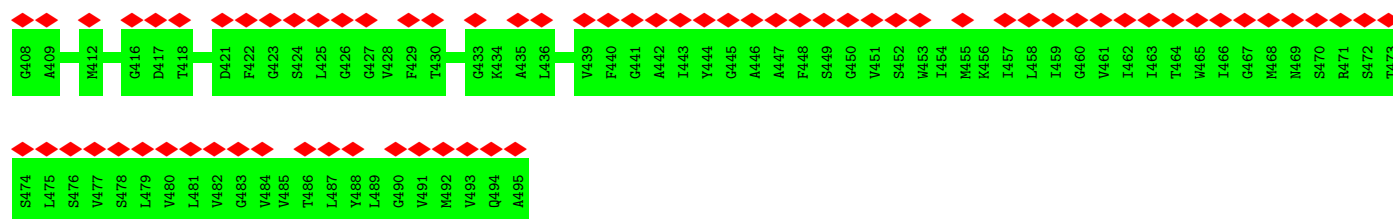
Chain C016:



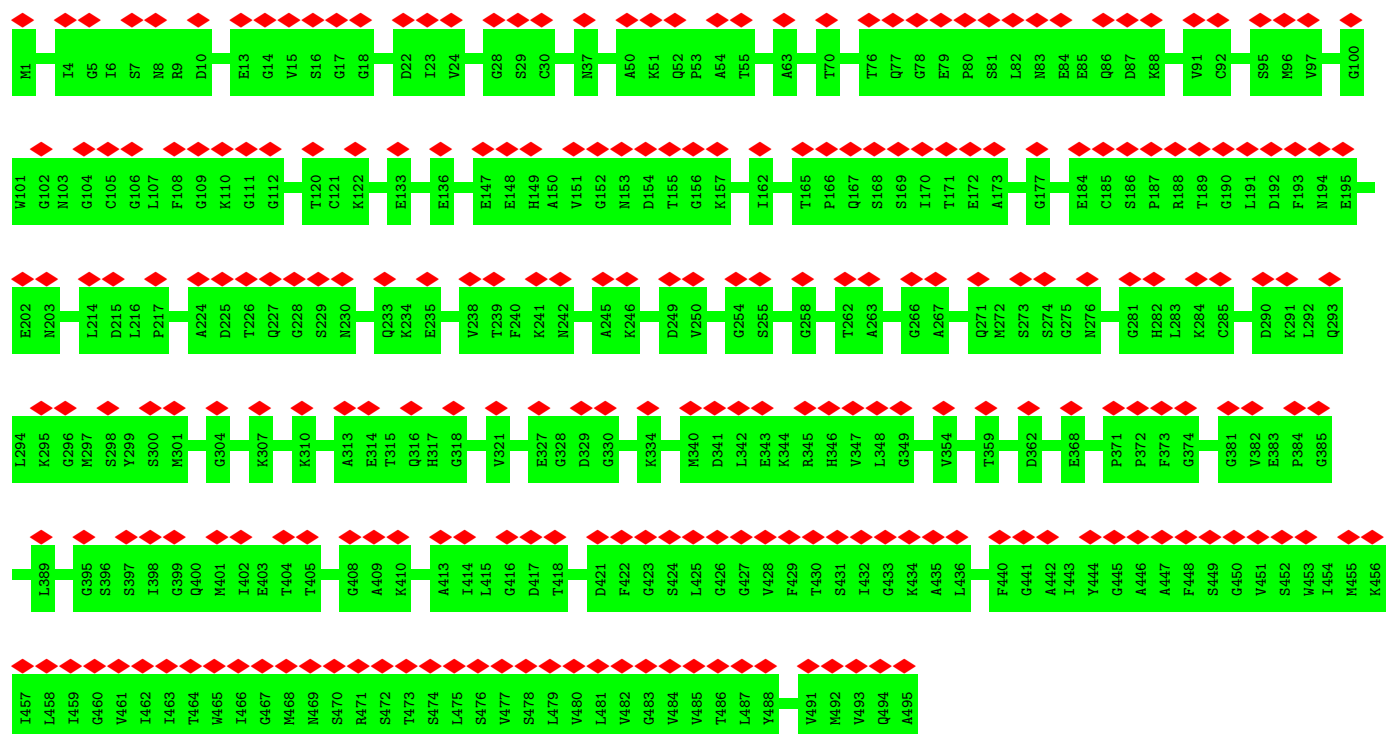
- Molecule 1: glycoprotein E

Chain A017:

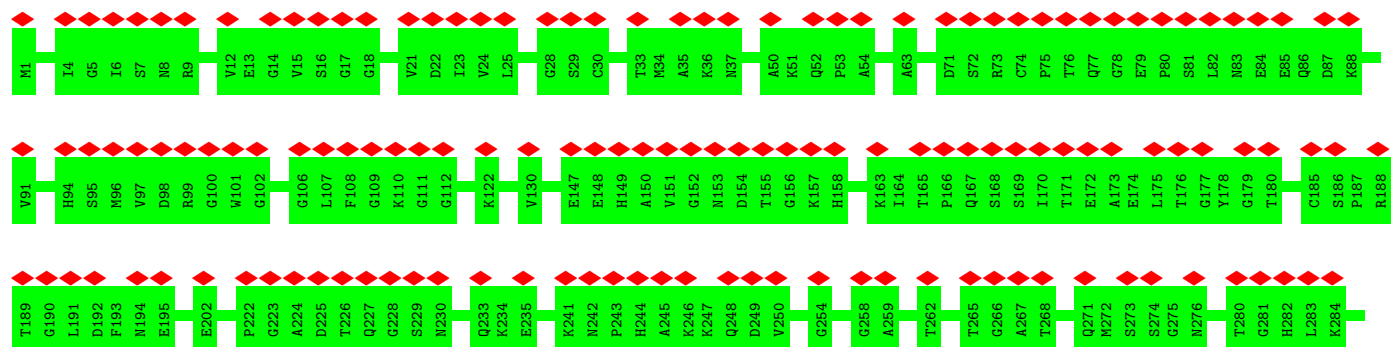


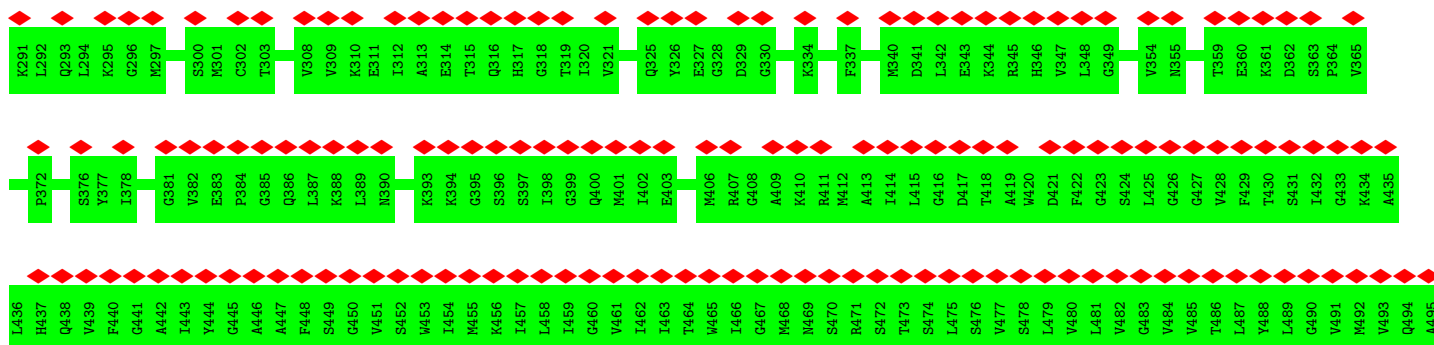


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

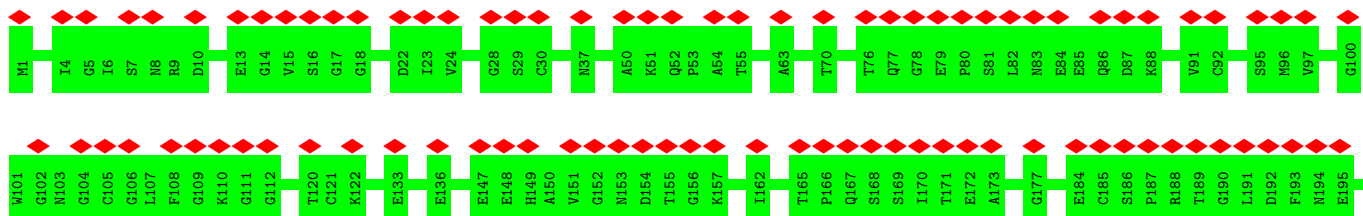


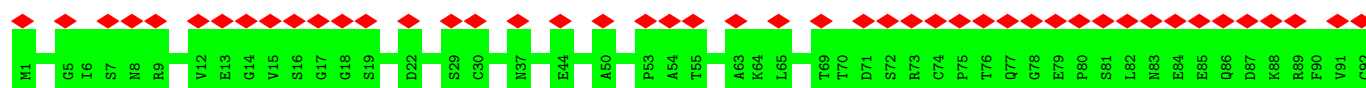


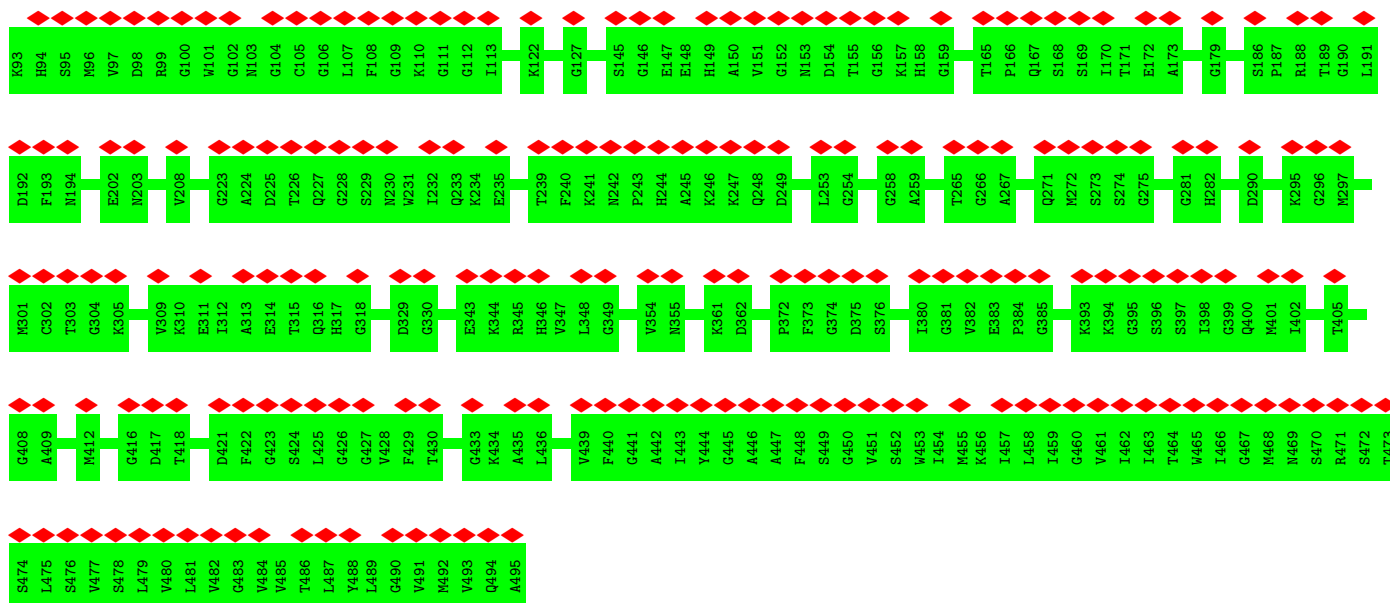
• Molecule 1: glycoprotein E



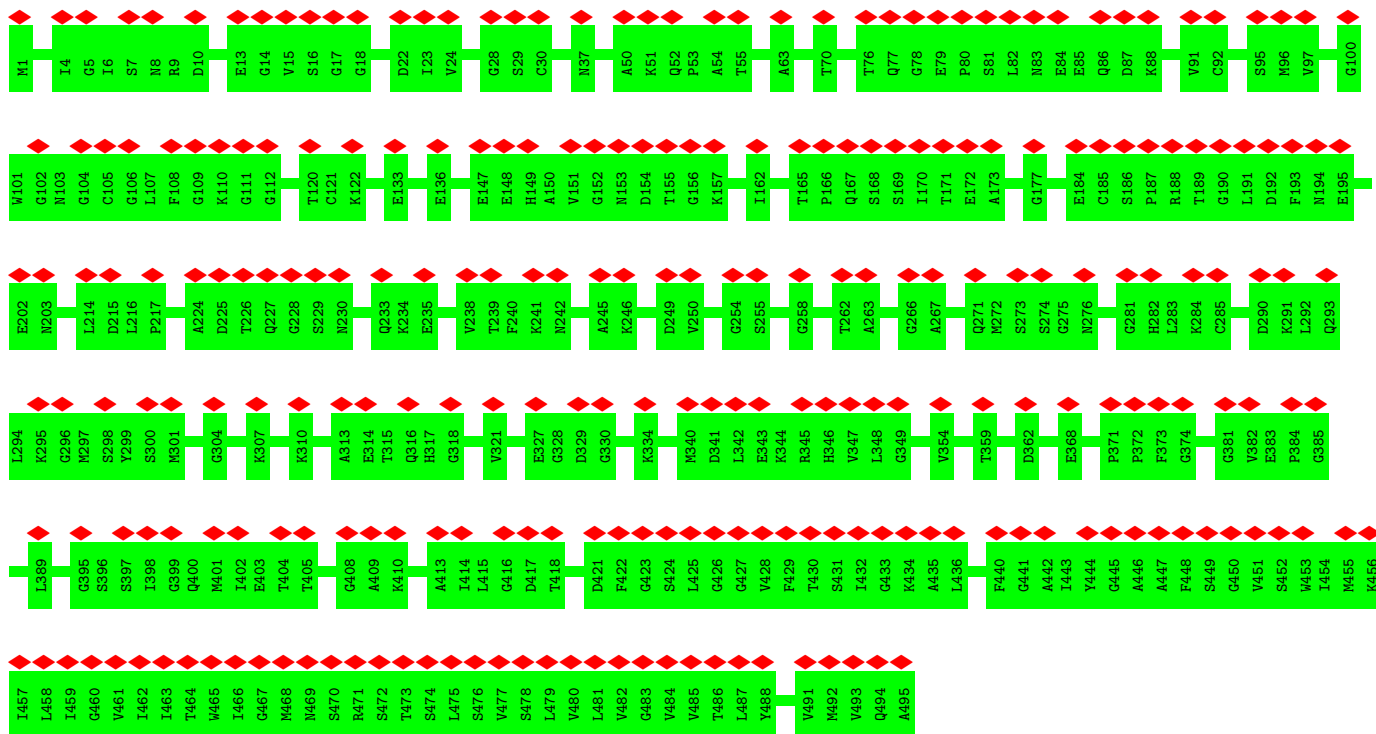
• Molecule 1: glycoprotein E







• Molecule 1: glycoprotein E

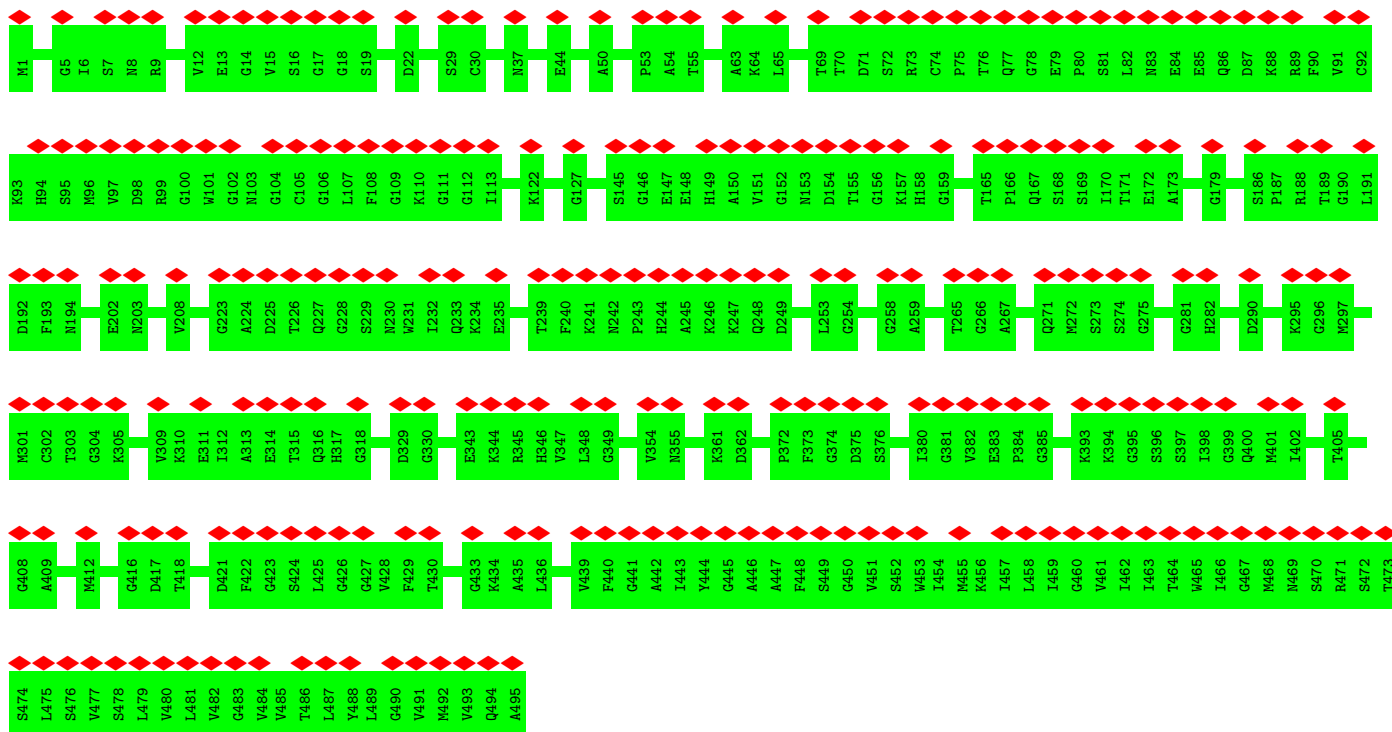


• Molecule 1: glycoprotein E





• Molecule 1: glycoprotein E



I457	L389	L294	E202	W101	M1
L458	G395 S396 S397	K295	W203	G102	I4
L459		K296	N103	G5	
G460		M297	G104	I6	
V461		S298	G105	S7	
I462	S397	Y299	L216	L107	N8
I463	I398	S300	P217	F108	R9
	G399	M301	A224 D225	G109	D10
T464	Q400	G304		K110	E13
W465	M401	K307	T226	G111	G14
I466	I402		Q227	G112	V15
G467	E403	K310	G228	T120	S16
M468	T404	A313	S229	C121	G17
M469	T405		W230	K122	G18
S470	G408	E314	Q233	E133	D22
R471	A409	T315	K234	E136	I23
S472	K410	H317	E235	E147 E148	V24
T473	A413	G318	V238		G28
S474		I414	V321	T239	S29
L475	L415	F240		H149	C30
S476	G416	E327	K241	N37	
V477	D417	G328	W242	A50	
S478	T418	D329	A245	K51	
L479	D421	G330	K246	Q52	
W480		F422	K334	A150	P53
L481	G423	S340		G151	A54
V482	G424	D341	V250	T55	
G483	S424	L342	G254	L162	A63
V484	L425	E343	S255	T165	T70
W485	G426	G427	G258	P166	T76
T486	V428	K344		T262	
L487	F429	T430	L346	G78	
V488	S431	I432	V347	E79	
	G433	K434	G349	P80	
V491	A435	L436	Q271	S81	
	M432	F440	M272	L82	
V493	G441	A442	S274	N83	
Q494	I443	Y444	G275	E84	
A495	G445	A446	W276	E85	
V498			P371	C185	Q86
	S449	F447	S186	D87	
V499	F448	L447	P187	K88	
	S449	G374	L188	V91	
G450	S449	G381	K284	C92	
V451	G450	V382	C285	G190	
S452	V451	E383	D290	L191	
W453	S452	P384	K291	D192	
I454	I454	G385	L292	F193	
K455	M455	G385	Q293	N194	
			E195	G100	

L436	H437	Q438	V439	F440	G441	A442	I443	V444	G445	A446	A447	F448	G449	V450	S451	S452	K393	K394	G395	S396	I397	I398	I399	Q400	M401	I402	E403	M406	R407	G408	A409	K410	N411	M412	A413	I414	L415	G416	D417	T418	A419	W420	D421	F422	G423	S424	L425	G426	G427	V428	F429	Y488	L489	G490	V491	M492	V493	Q494
P372	S376	Y377	I378	G381	V382	E383	P384	G385	Q386	L387	K388	L389	N390	K393	K394	G395	S396	I397	I398	I399	Q400	M401	I402	E403	M406	R407	G408	A409	K410	N411	M412	A413	I414	L415	G416	D417	T418	A419	W420	D421	F422	G423	S424	L425	G426	G427	V428	F429	Y488	L489	G490	V491	M492	V493	Q494			
K291	L292	Q293	L294	K295	G296	M297	S300	M301	C302	T303	V308	V309	K310	E311	I312	A313	E314	T315	Q316	H317	G318	T319	I320	V321	Q325	Y326	E327	G328	D329	G330	K334	F337	K340	D341	L342	E343	K344	R345	H346	V347	L348	G349	V354	N355	T359	E360	K361	D362	S363	P364	V365							
T189	G190	L191	D192	F193	N194	E195	E202	P222	G223	A224	D225	T226	Q227	G228	S229	M230	Q233	K234	E235	K241	N242	P243	H244	A245	K246	R247	Q248	D249	V250	G254	G258	A259	T262	T265	G266	A267	T268	Q271	R272	S273	S274	G275	H276	T280	G281	H282	L283	K284										
V91	H94	S95	H96	V97	D98	R99	G100	W101	G102	G106	L107	F108	G109	K110	G111	G112	K122	V130	E147	E148	H149	A150	V151	G152	N153	D154	T155	G156	K157	H158	K163	I164	T165	P166	Q167	S168	S169	I170	T171	E172	A173	E174	L175	T176	G177	L178	G179	T180	C185	S186	P187	R188						
M1	I4	G5	I6	S7	N8	R9	V12	E13	G14	V15	S16	G17	G18	V21	D22	L23	V24	L26	G28	S29	C30	T33	M34	A35	K36	N37	A50	K51	Q52	P53	A54	A63	D71	S72	R73	G74	P75	T76	Q77	G78	E79	P80	S81	L82	N83	E84	Q85	R86	D87	K88								

- Molecule 1: glycoprotein E

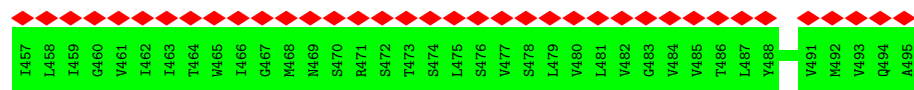
Chain C021:



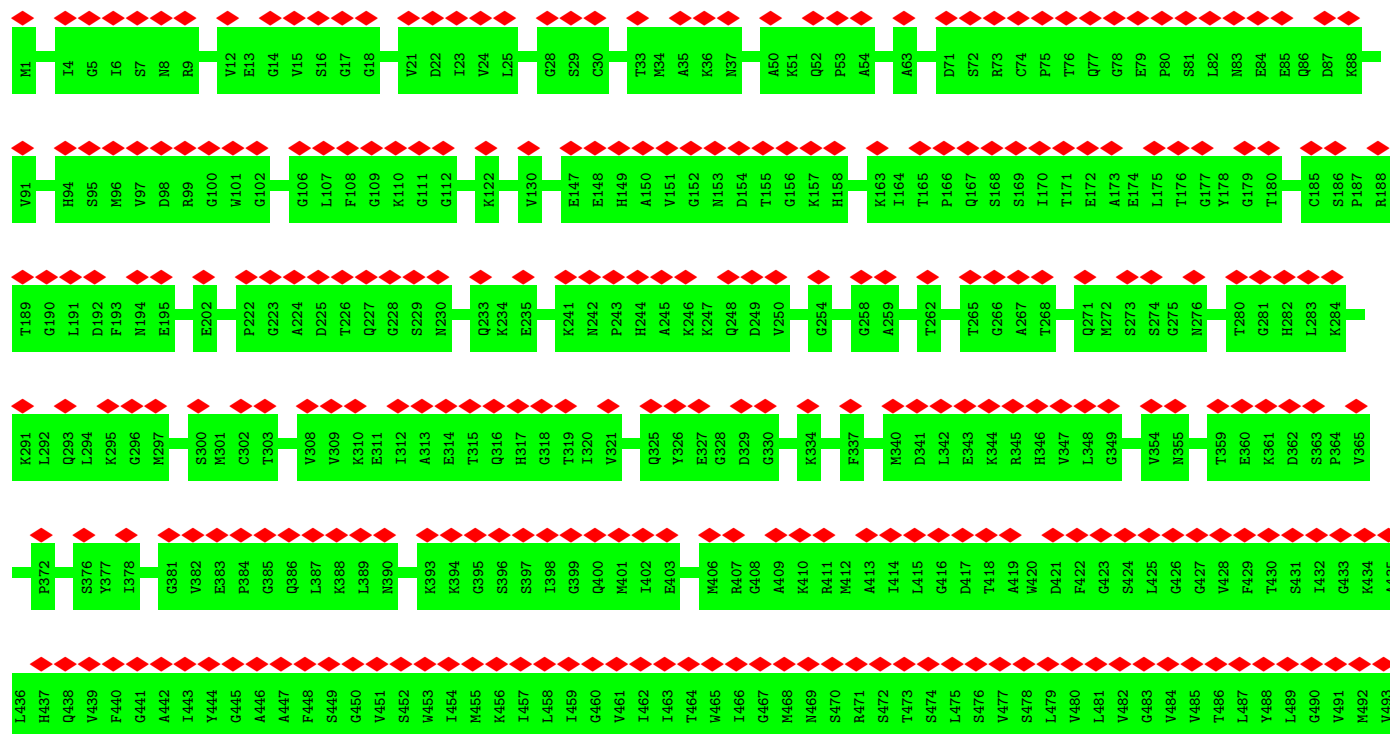
- Molecule 1: glycoprotein E

Chain A022:

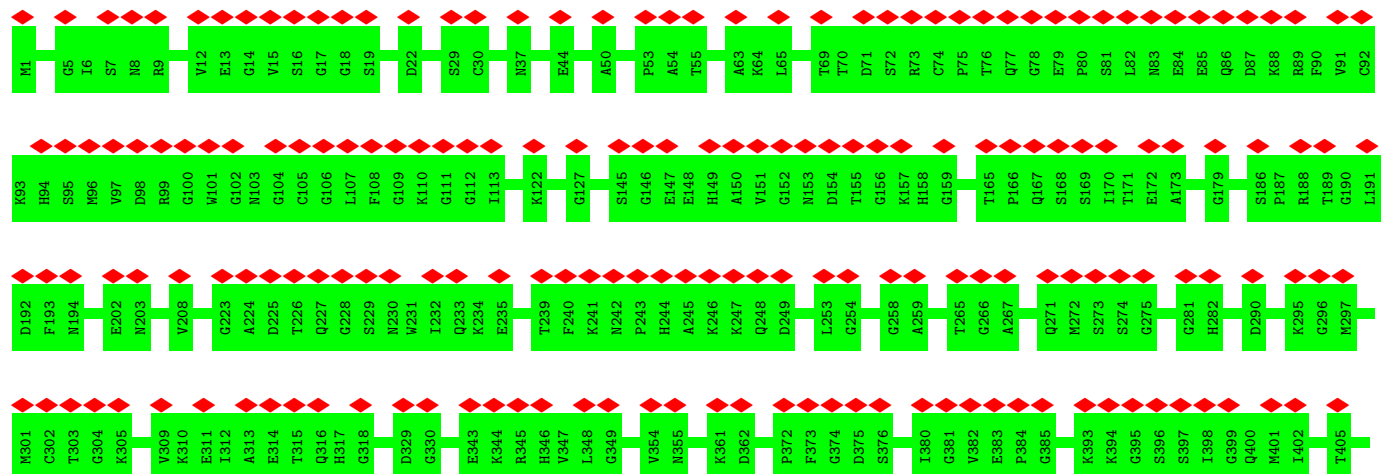


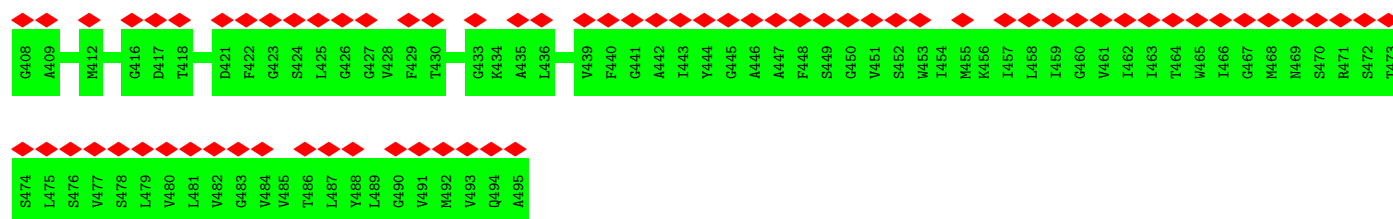


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

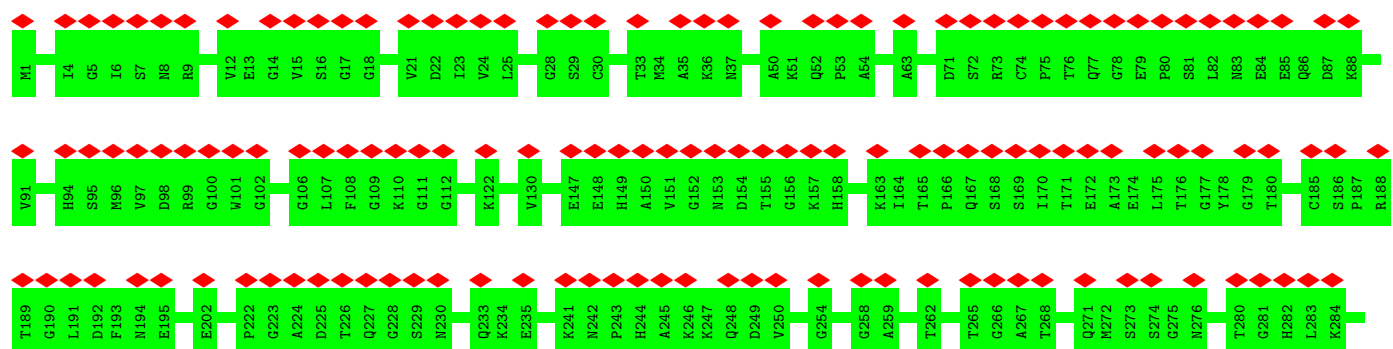


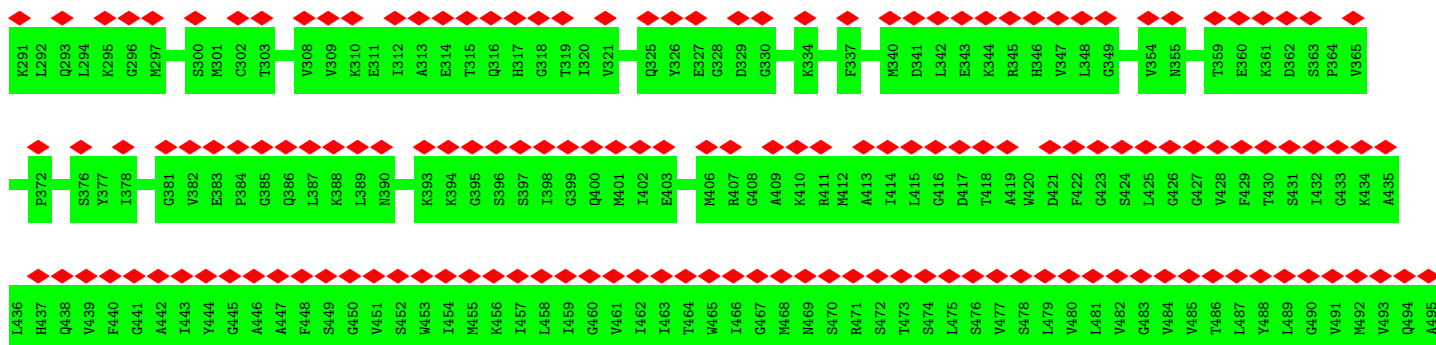


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

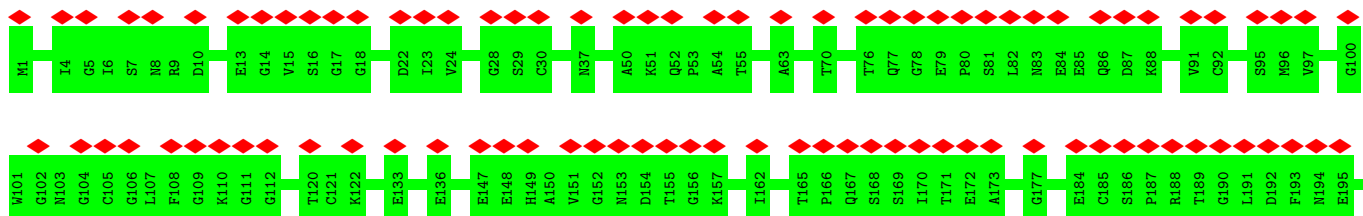


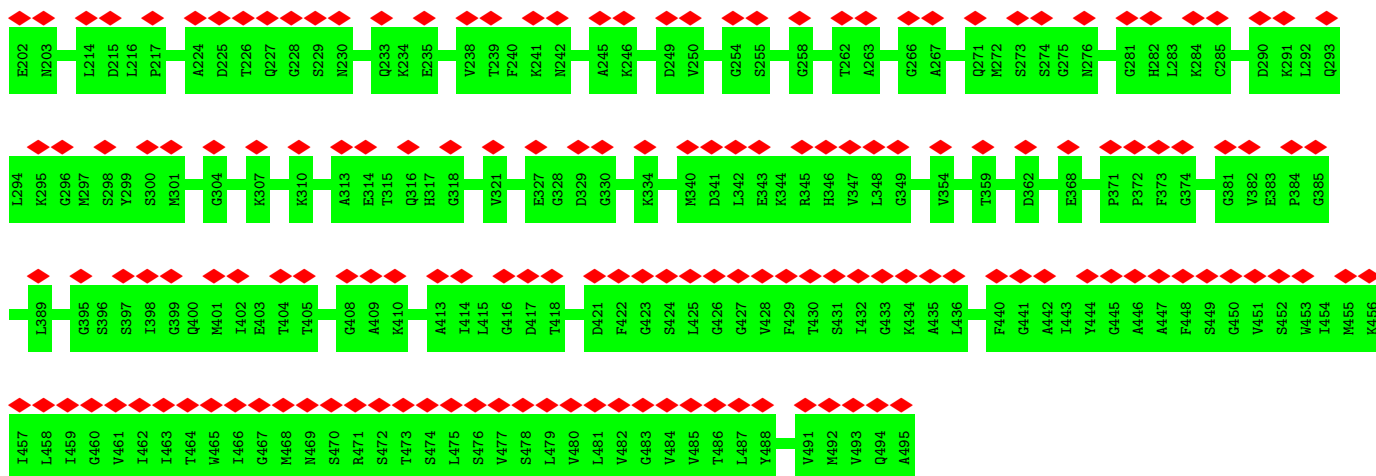


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

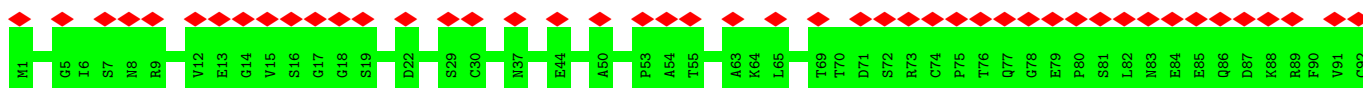


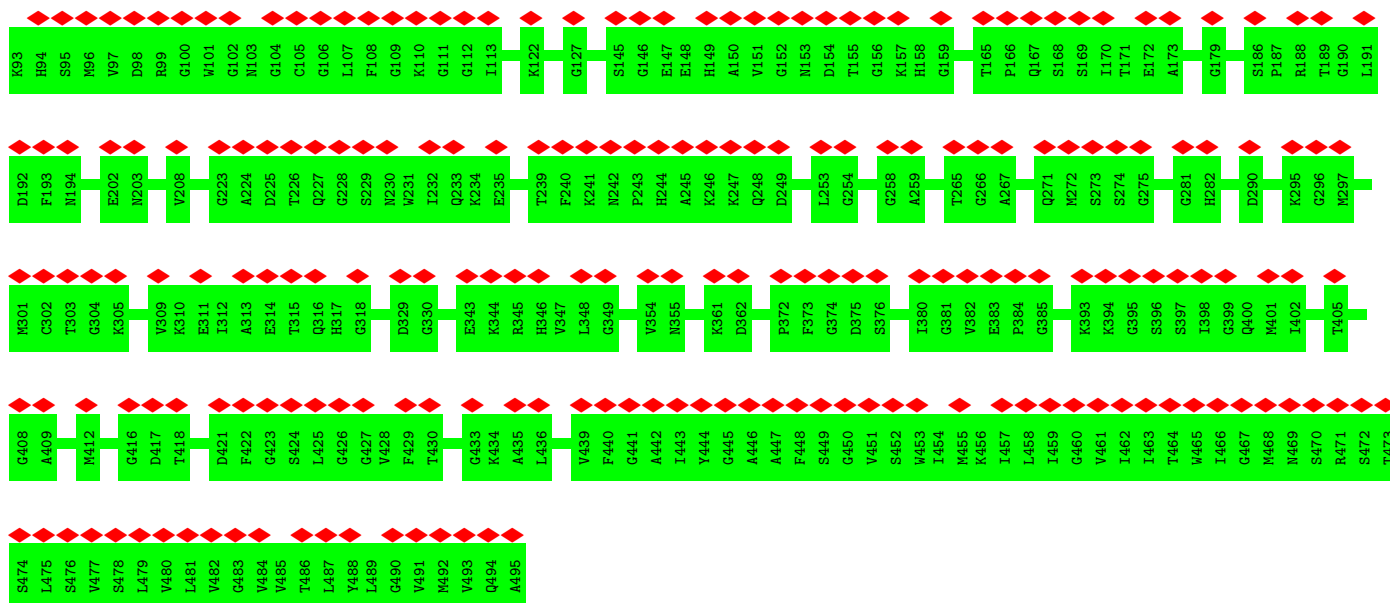


• Molecule 1: glycoprotein E

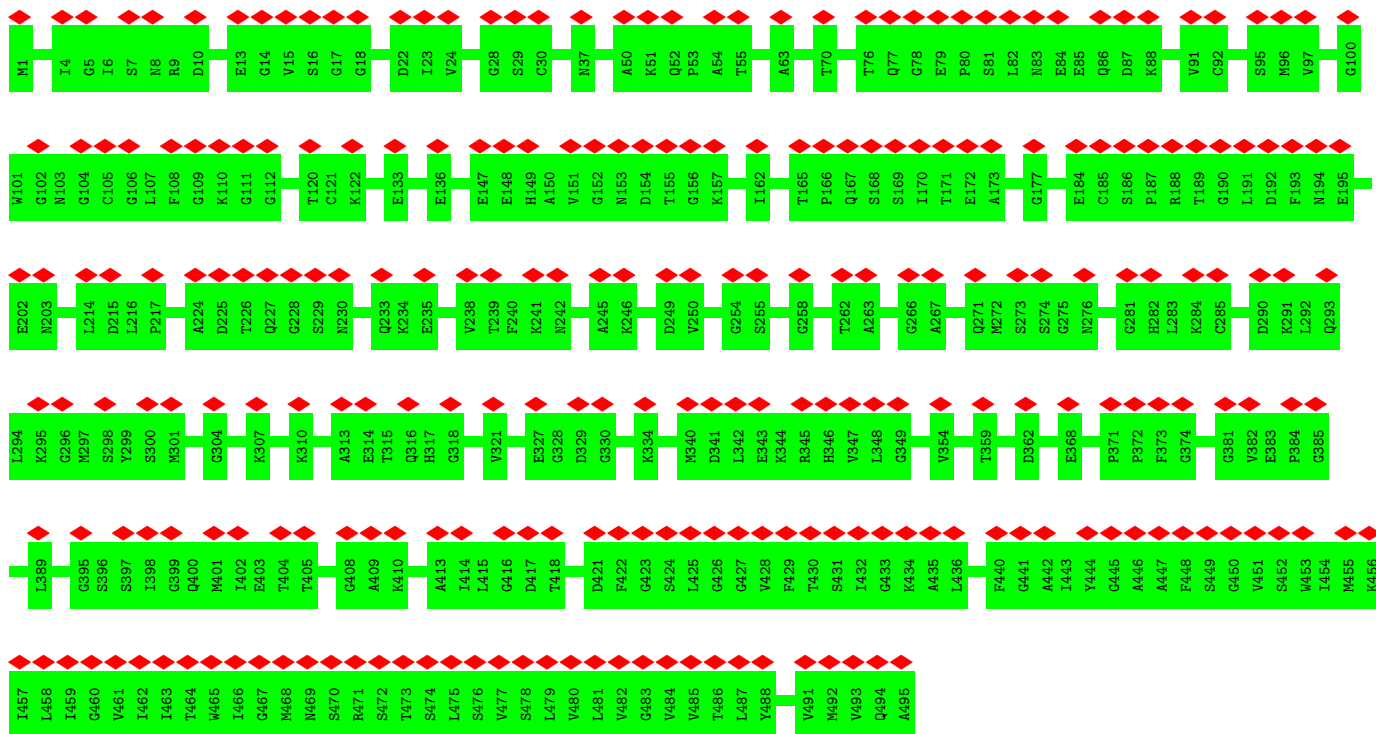


• Molecule 1: glycoprotein E



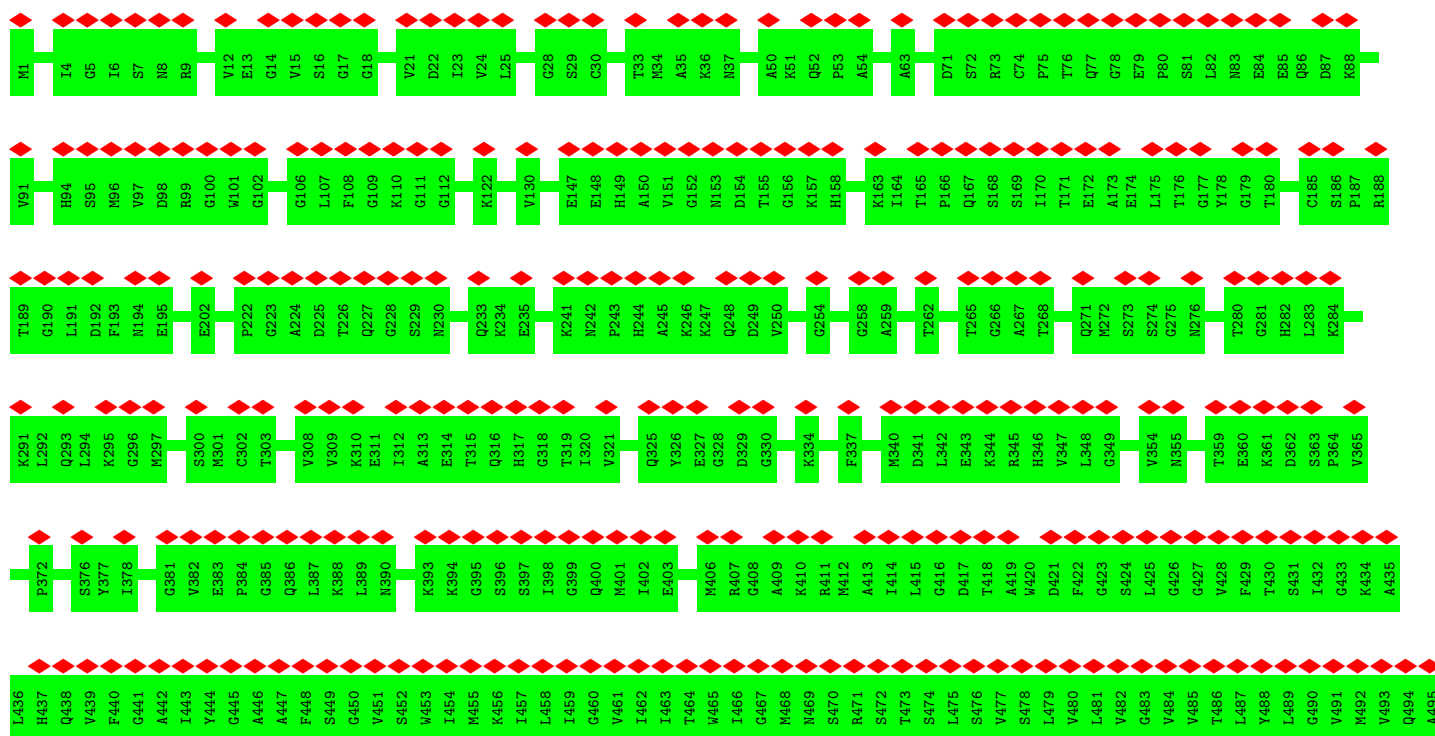


• Molecule 1: glycoprotein E



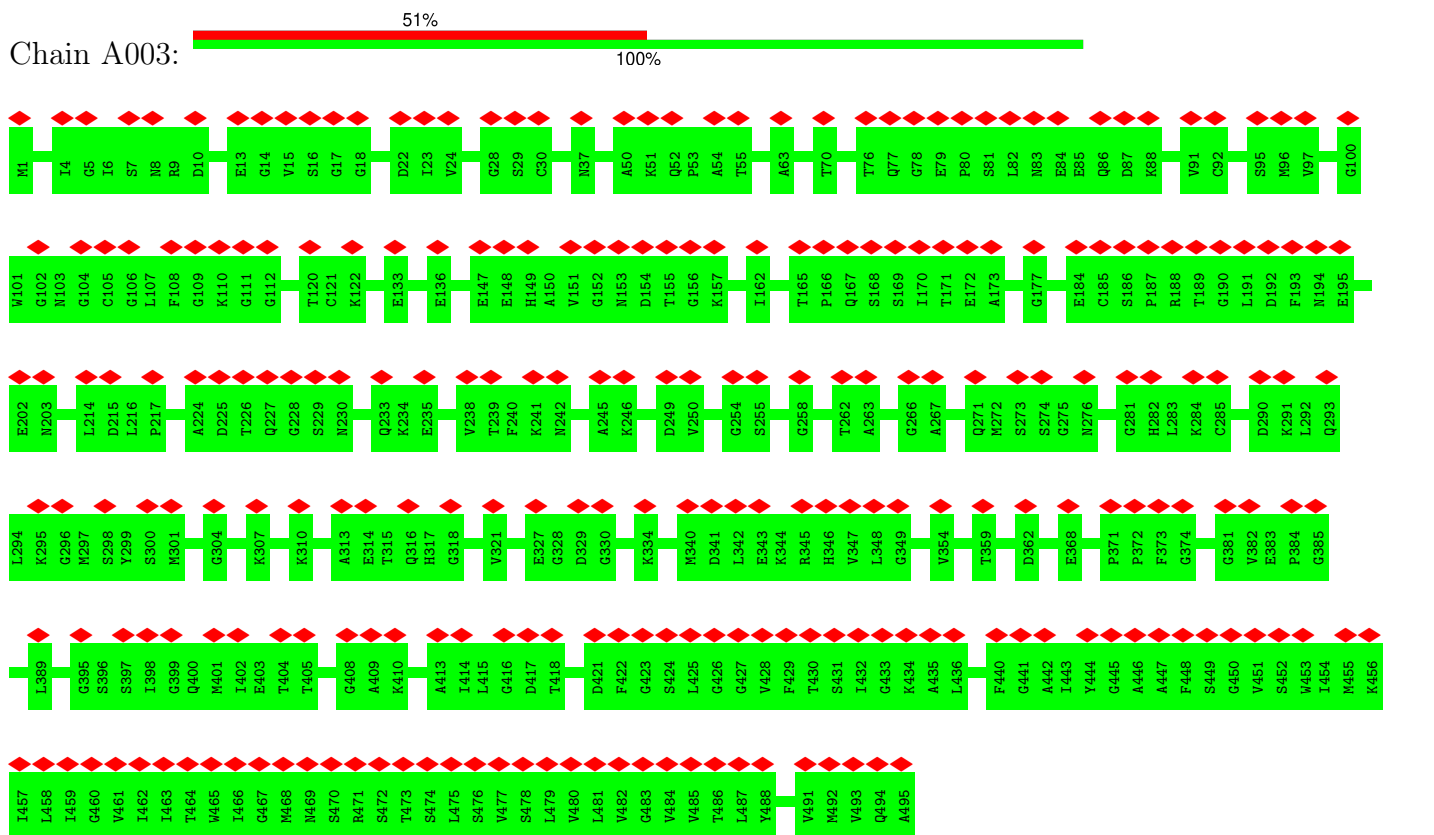
• Molecule 1: glycoprotein E





- Molecule 1: glycoprotein E



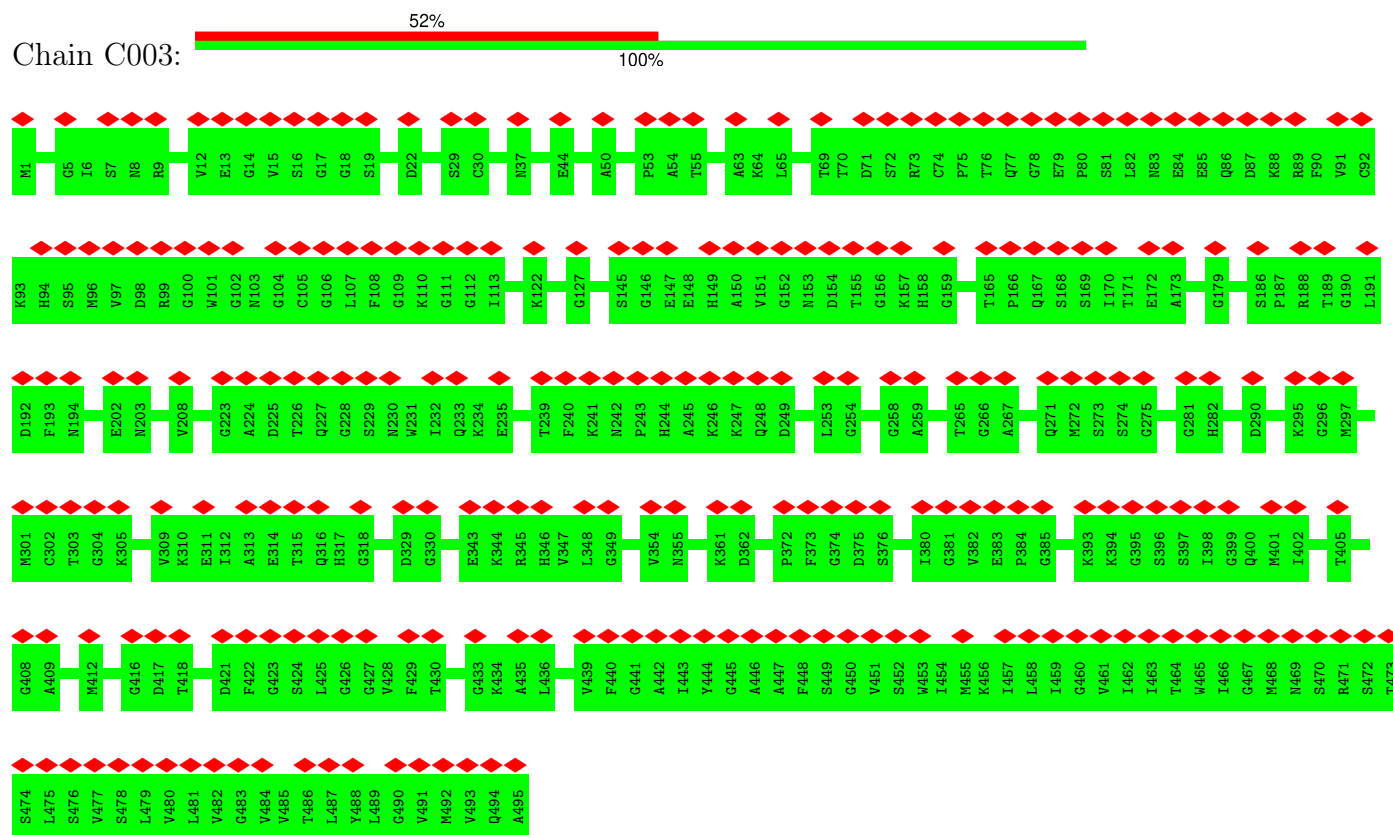


- Molecule 1: glycoprotein E



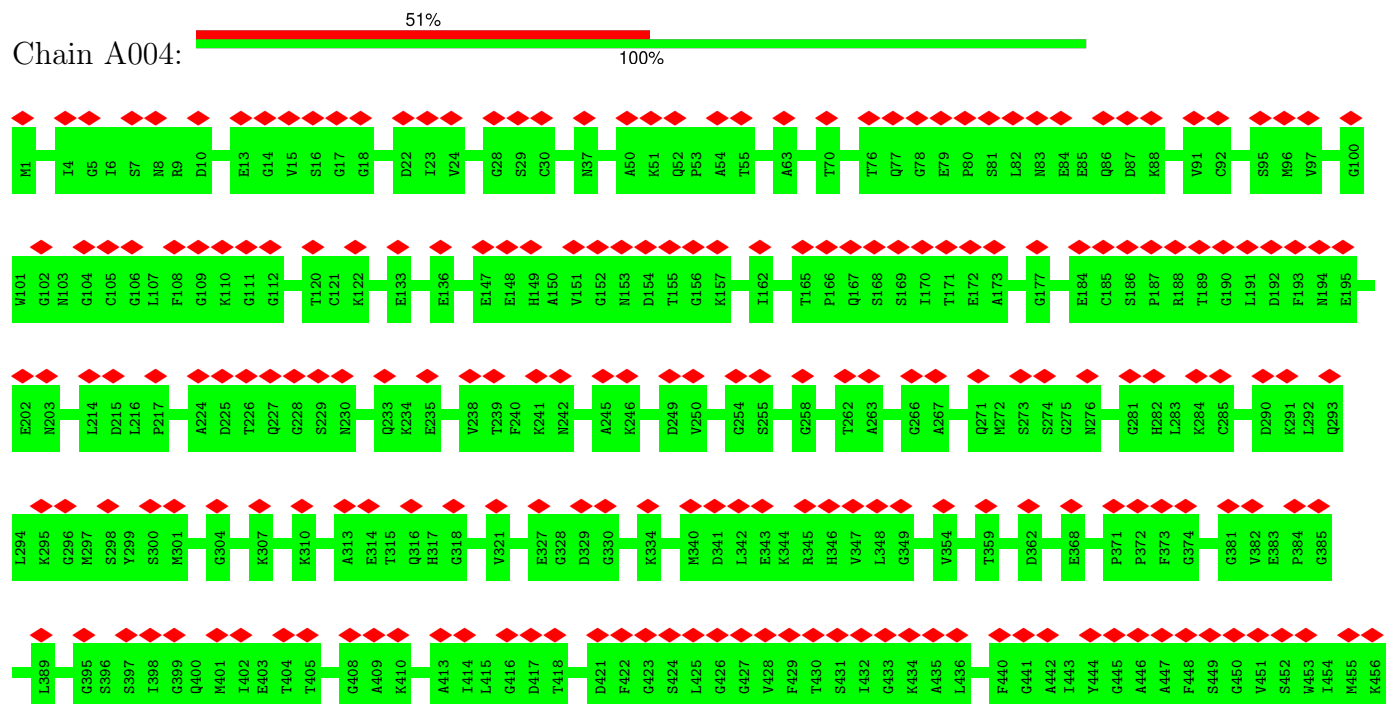
- Molecule 1: glycoprotein E

Chain C003:



- Molecule 1: glycoprotein E

Chain A004:

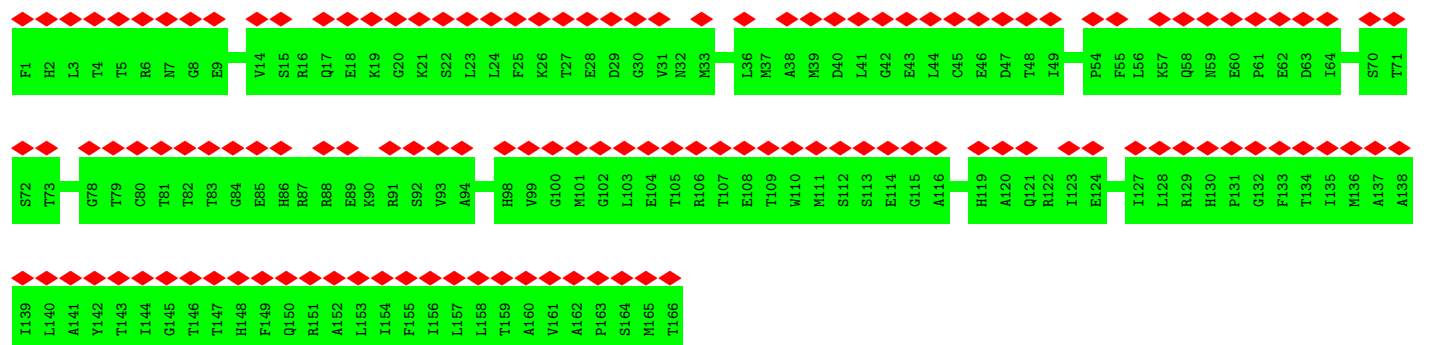
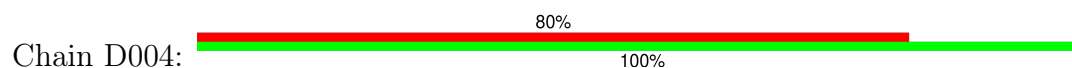




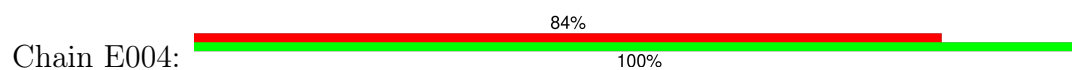
• Molecule 1: glycoprotein E

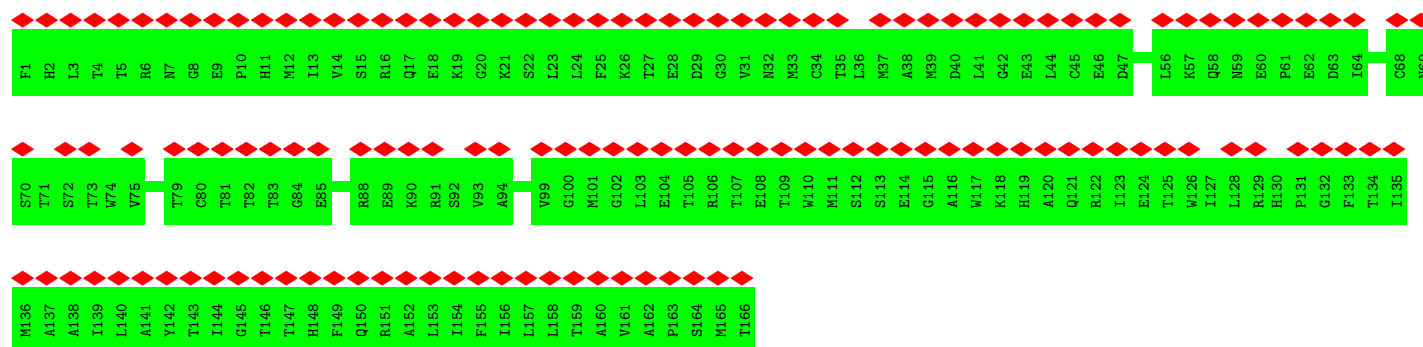


• Molecule 2: Protein prM

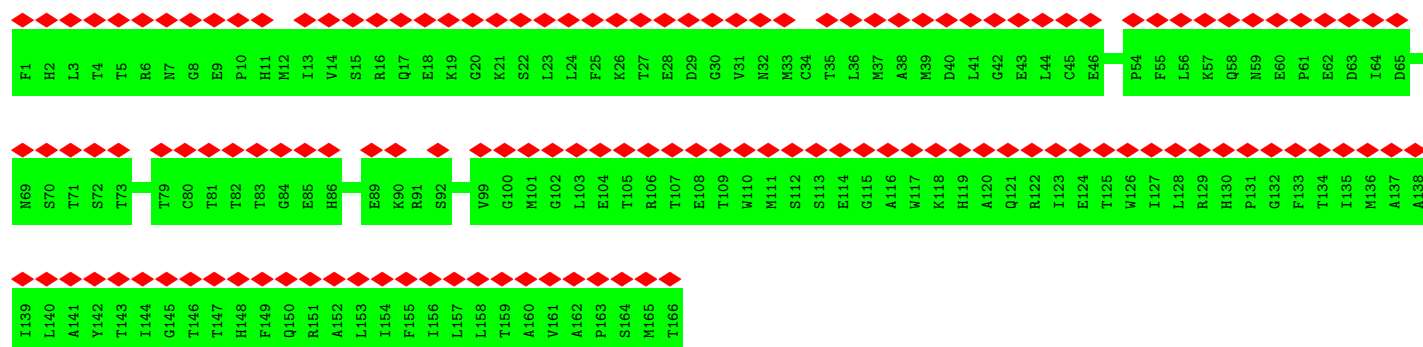


• Molecule 2: Protein prM

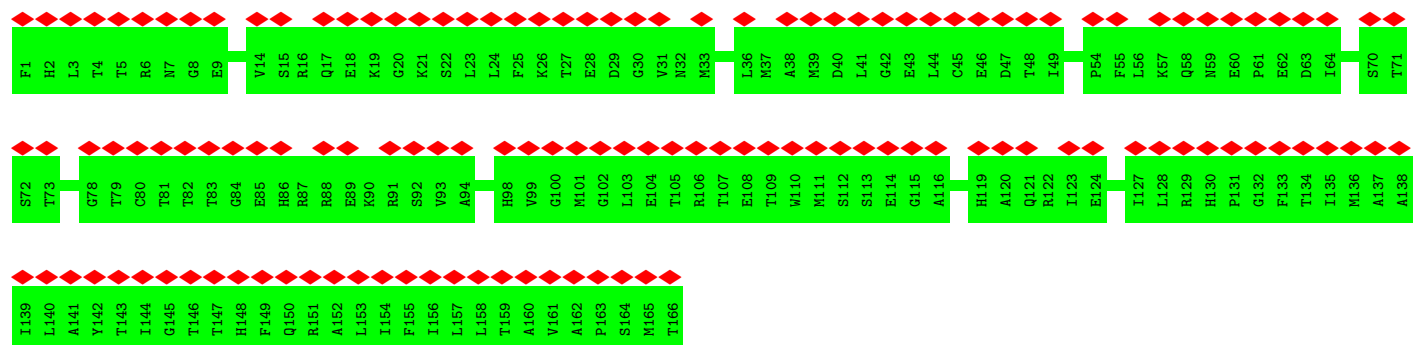
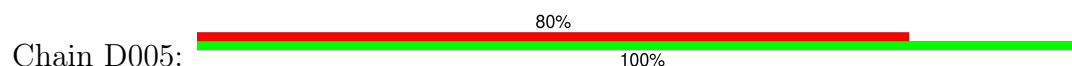




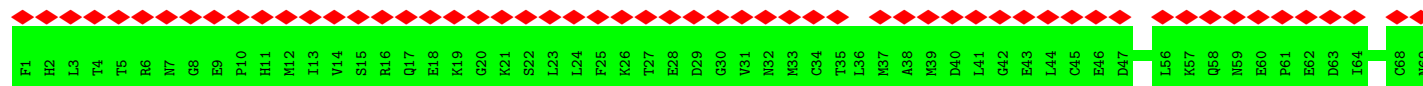
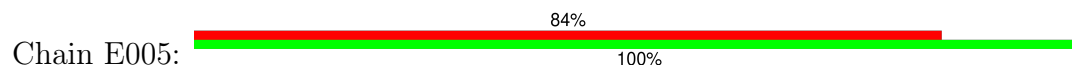
• Molecule 2: Protein prM

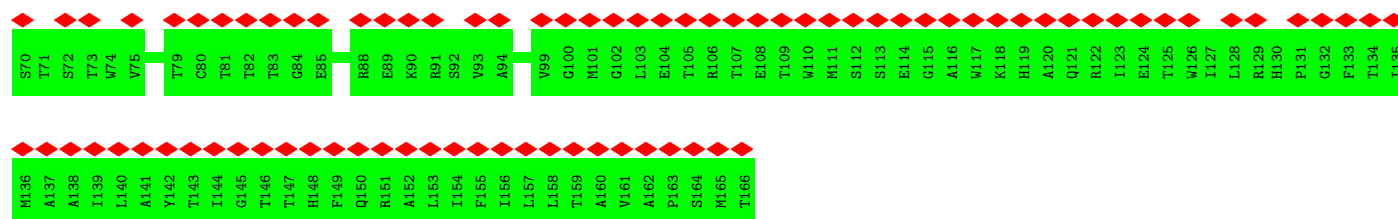


• Molecule 2: Protein prM

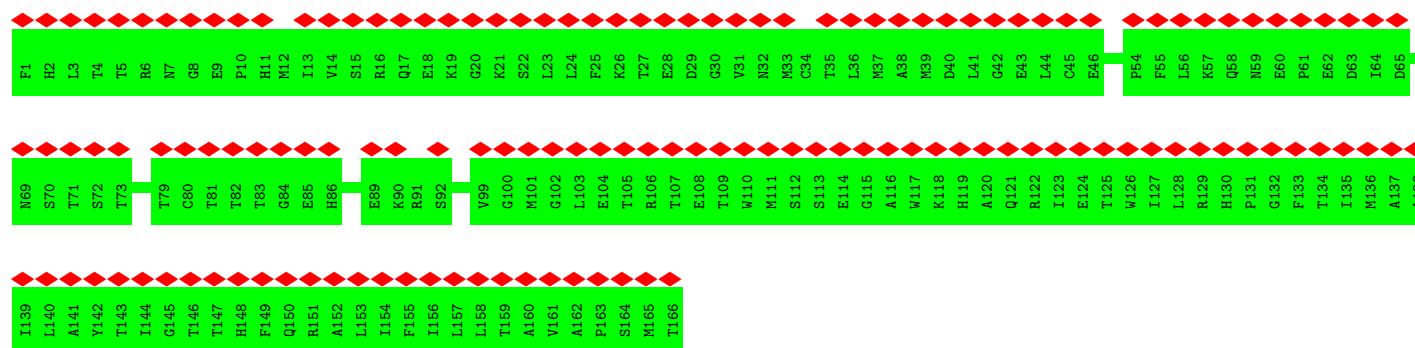
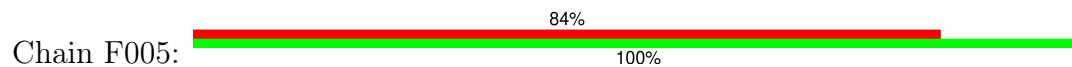


• Molecule 2: Protein prM

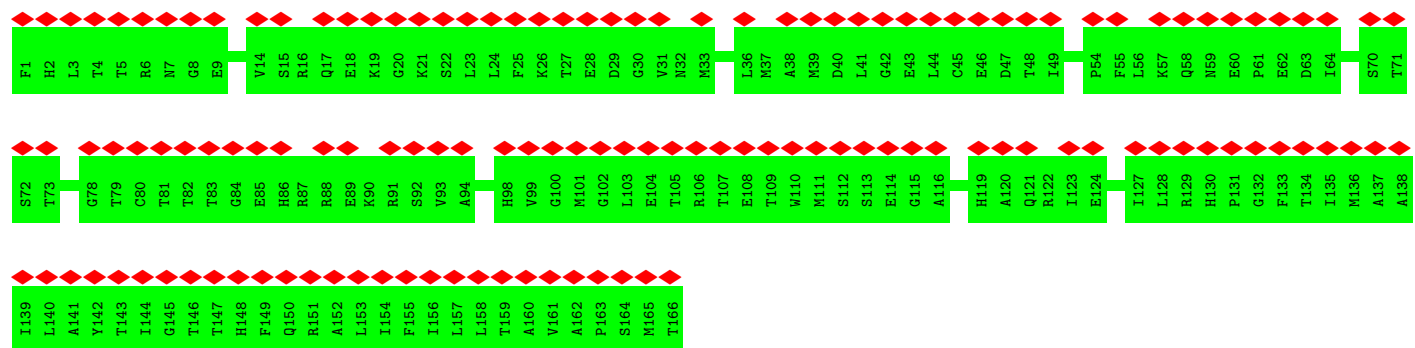
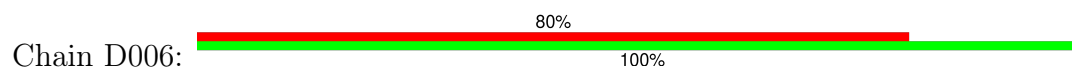




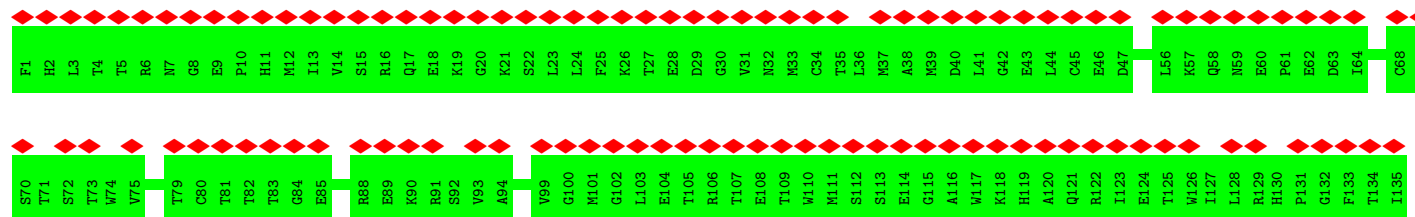
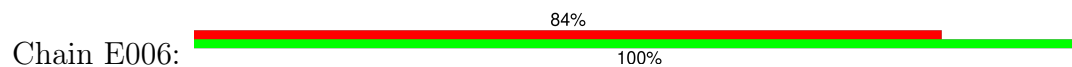
• Molecule 2: Protein prM

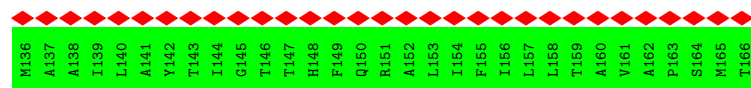


• Molecule 2: Protein prM

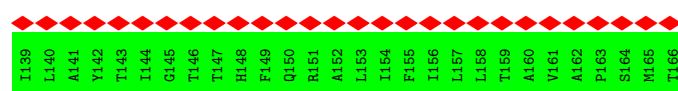
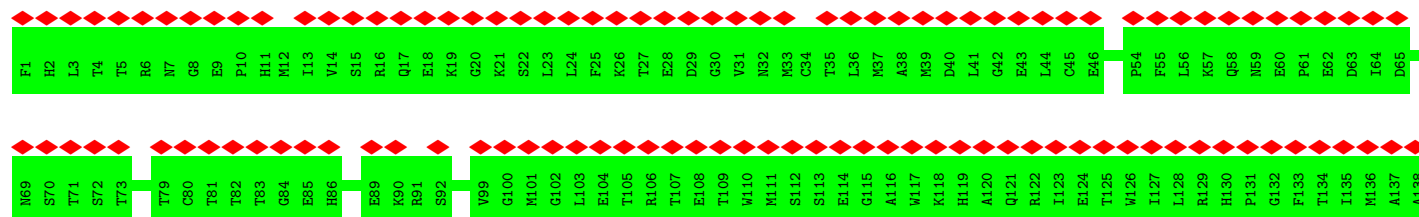
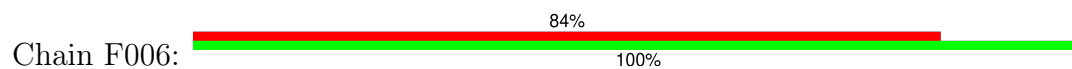


• Molecule 2: Protein prM

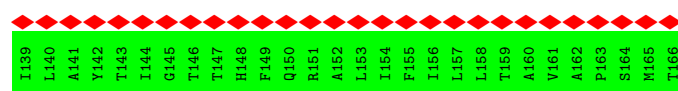
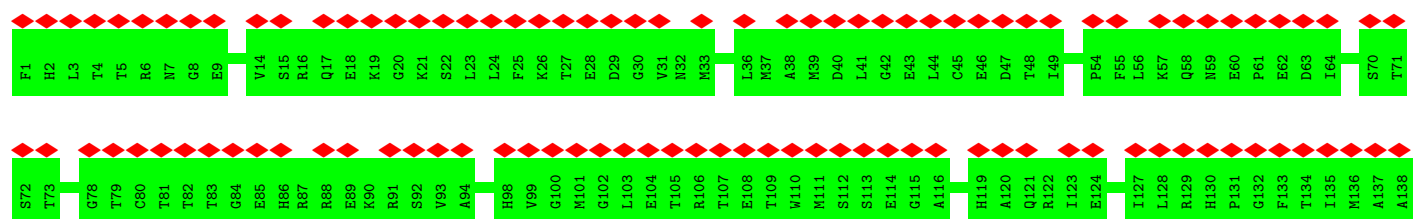
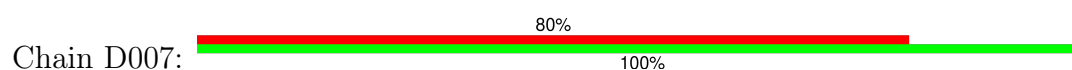




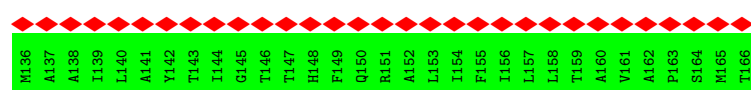
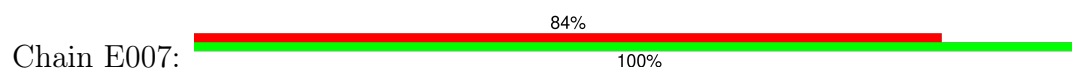
• Molecule 2: Protein prM



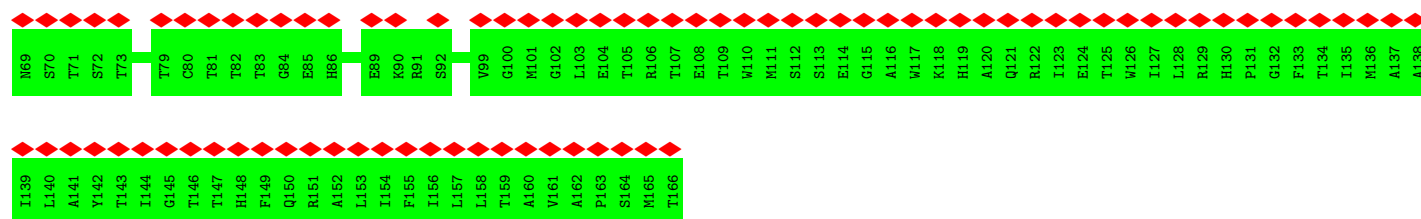
• Molecule 2: Protein prM



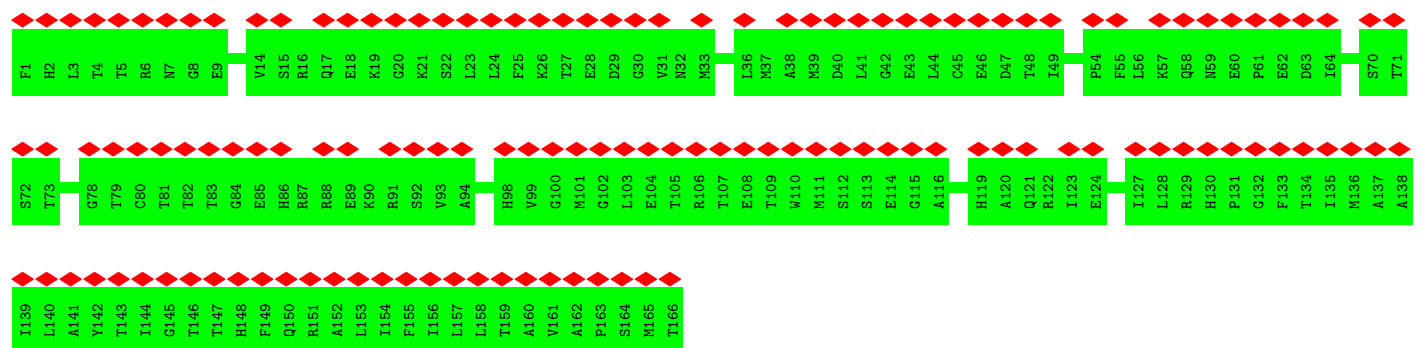
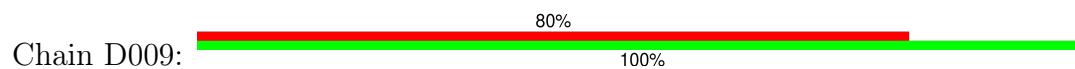
• Molecule 2: Protein prM



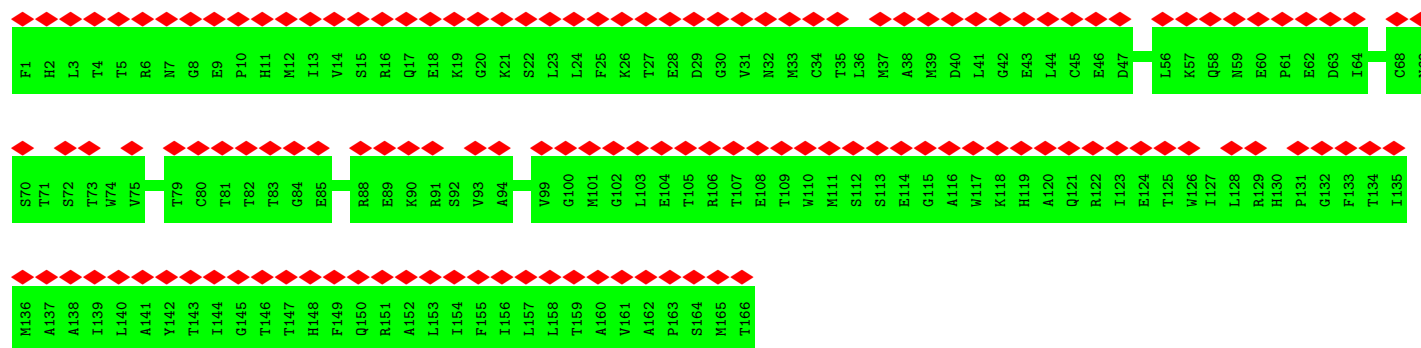
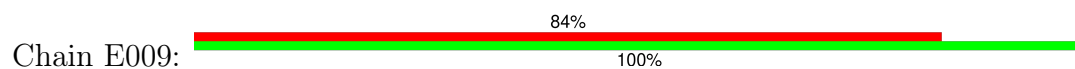
• Molecule 2: Protein prM



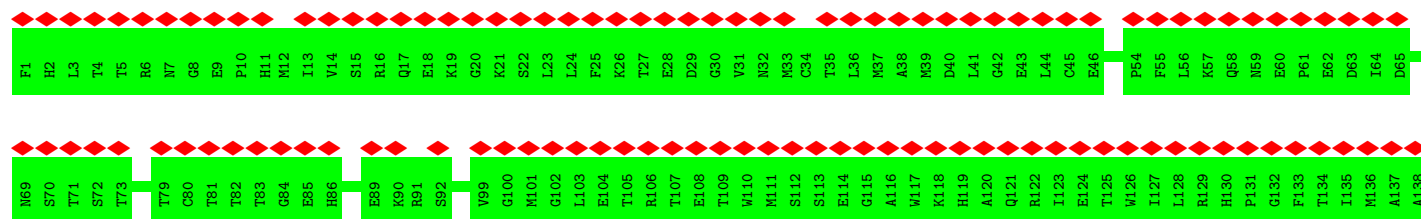
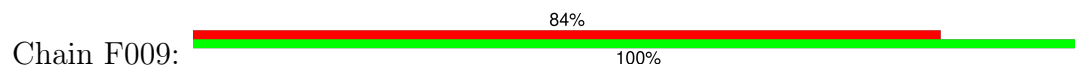
• Molecule 2: Protein prM



• Molecule 2: Protein prM

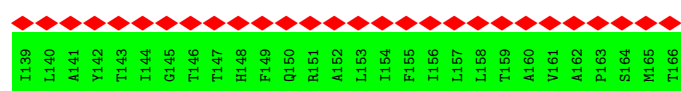
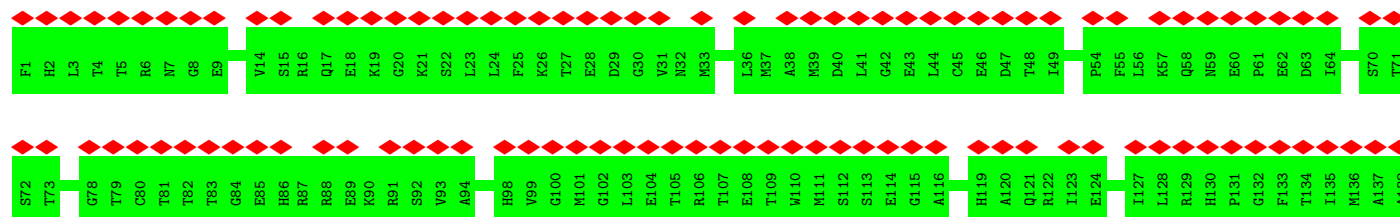
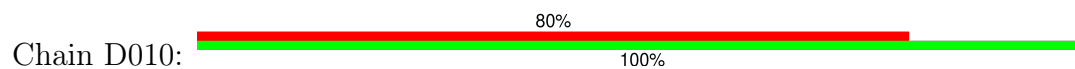


• Molecule 2: Protein prM

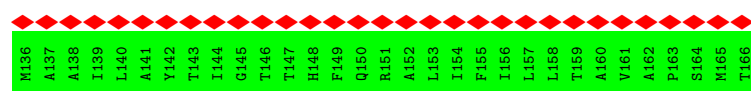
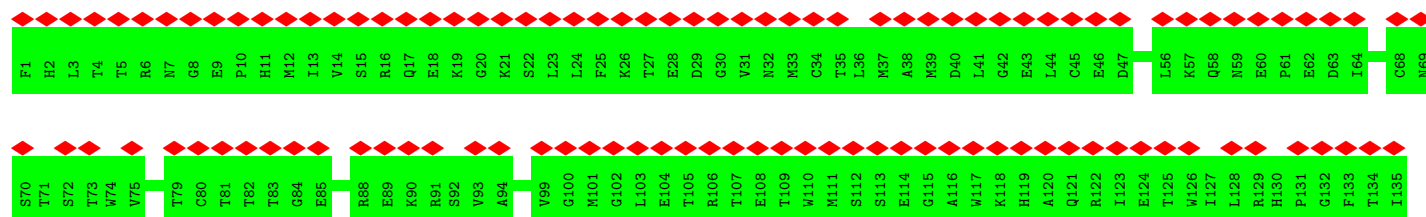
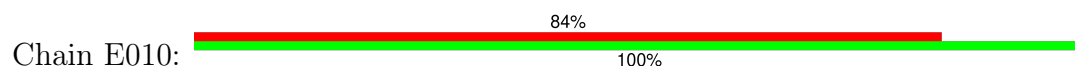




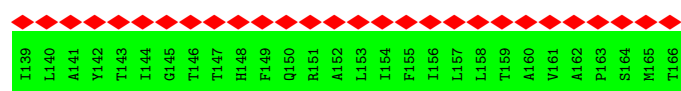
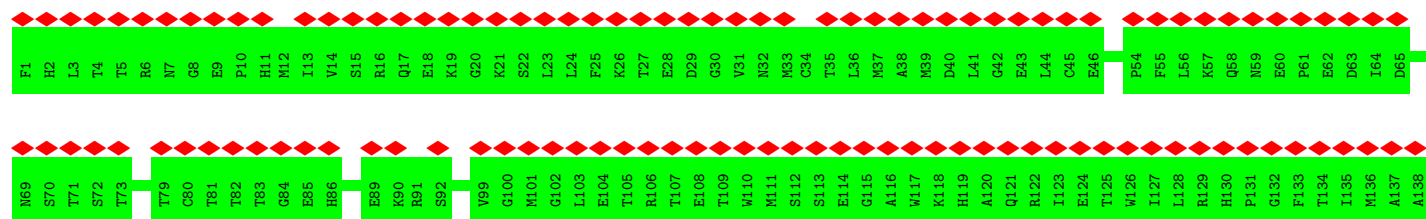
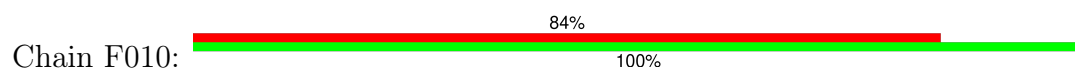
• Molecule 2: Protein prM



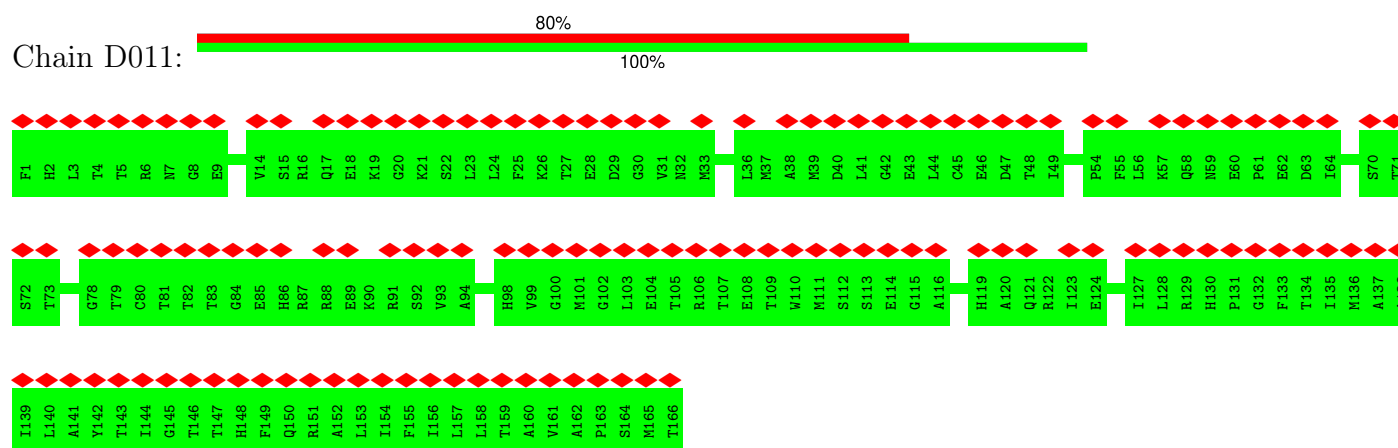
• Molecule 2: Protein prM



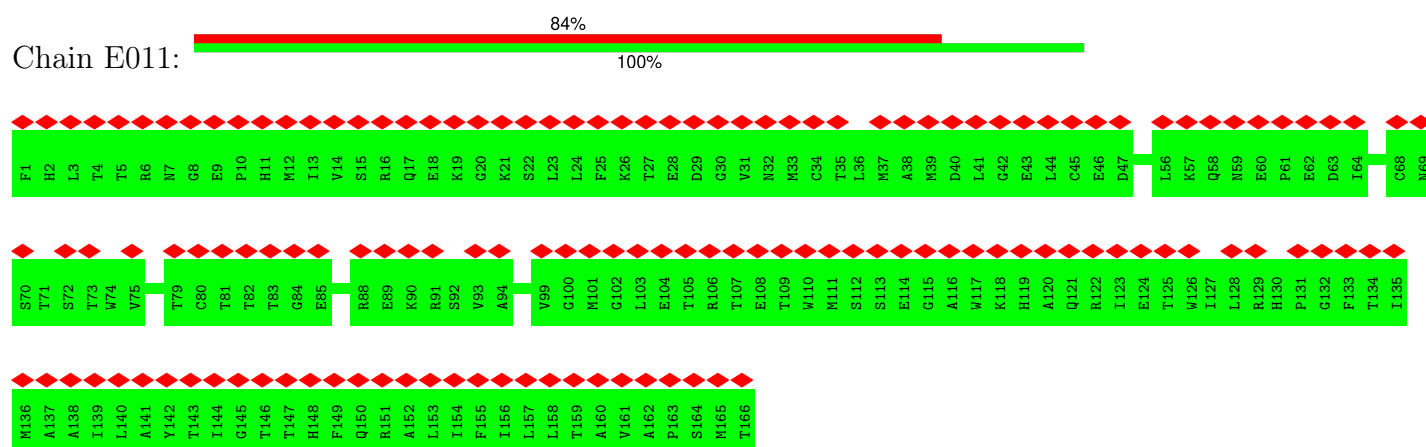
• Molecule 2: Protein prM



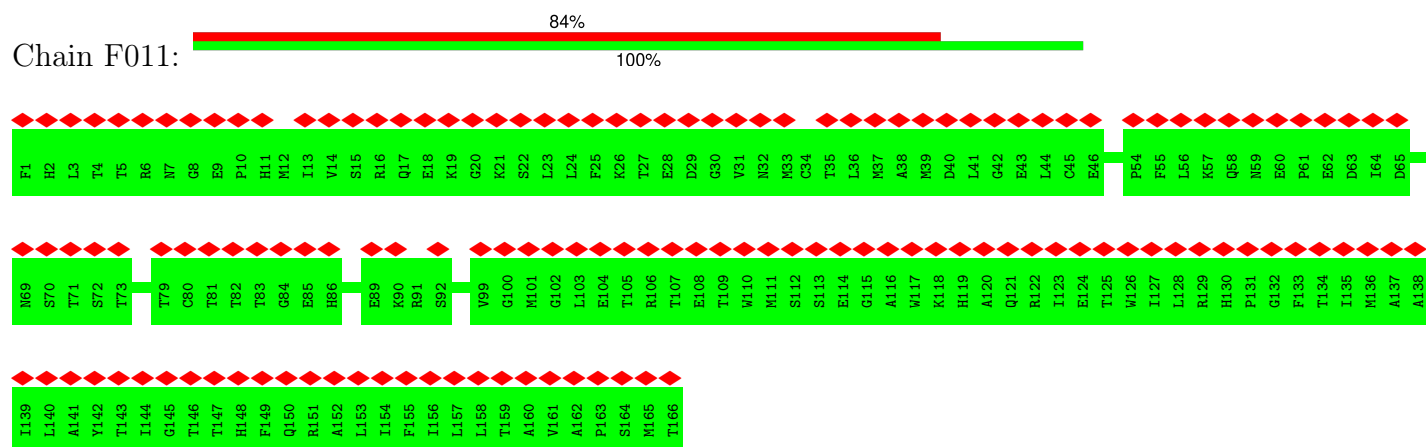
• Molecule 2: Protein prM



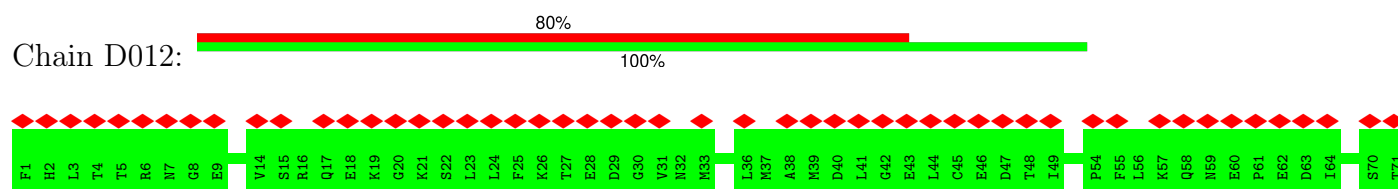
- Molecule 2: Protein prM

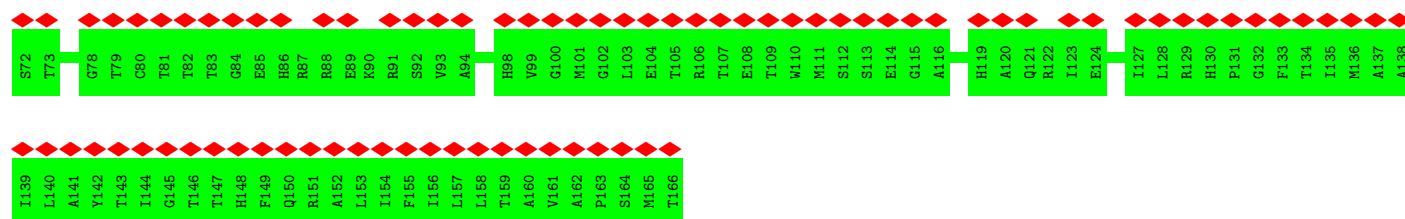


- Molecule 2: Protein prM

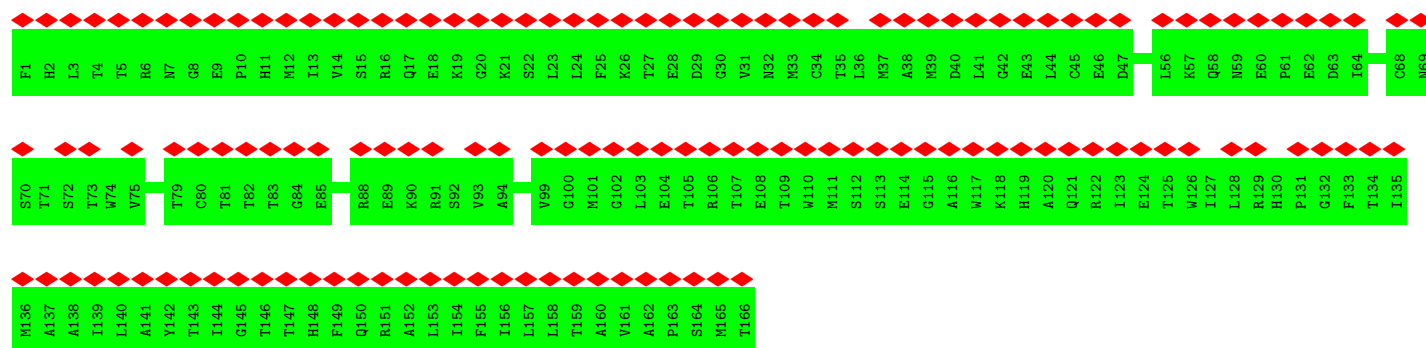
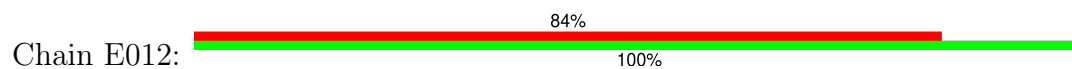


- Molecule 2: Protein prM

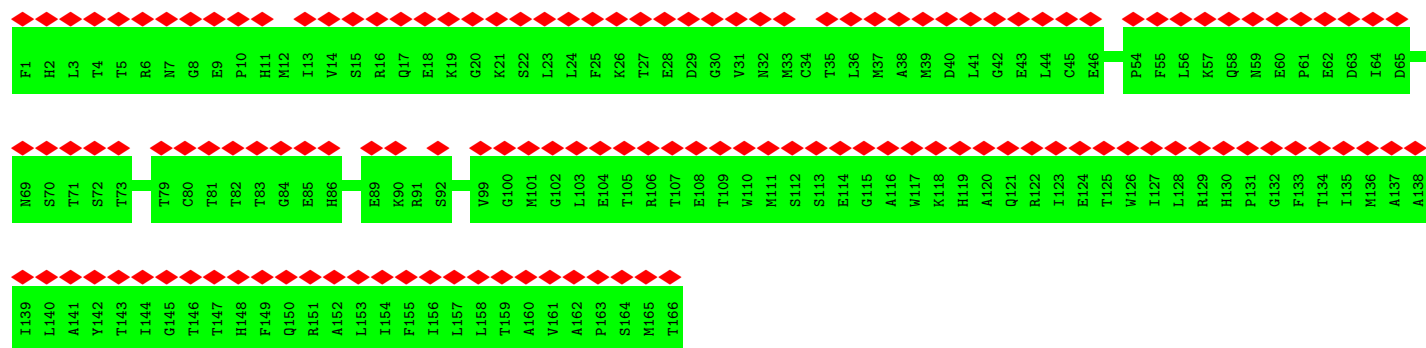
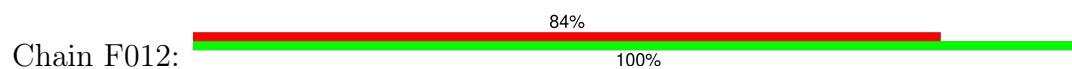




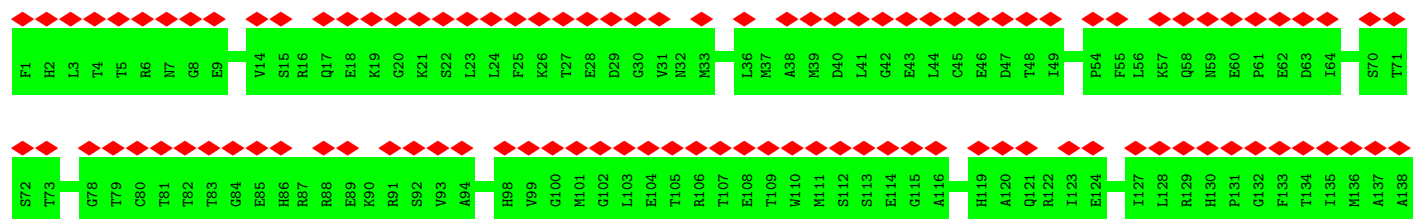
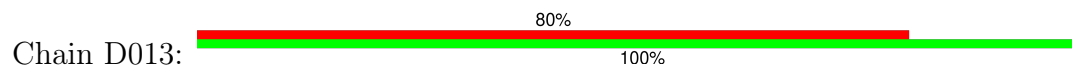
- Molecule 2: Protein prM



- Molecule 2: Protein prM

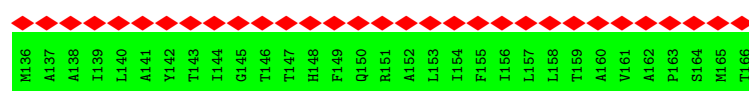
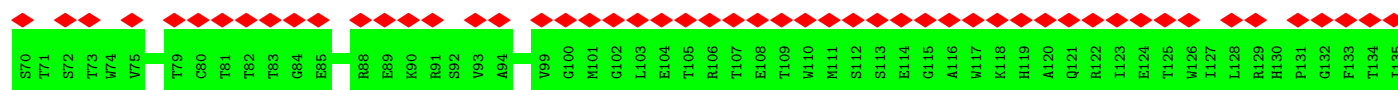
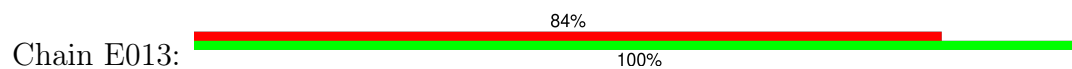


- Molecule 2: Protein prM

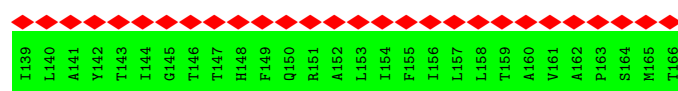
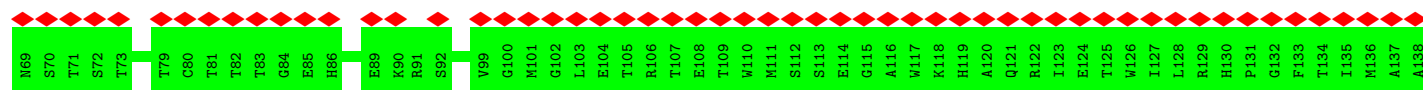
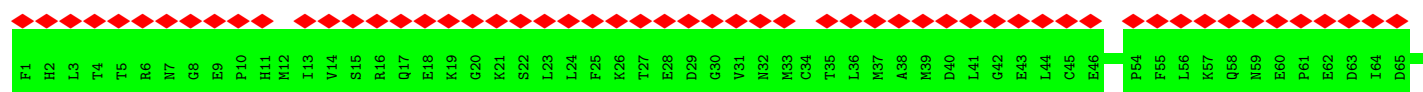
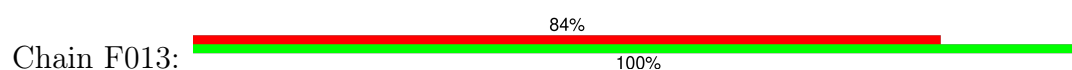




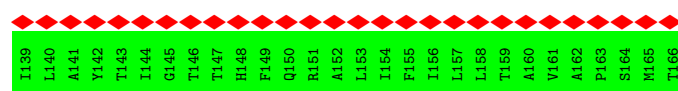
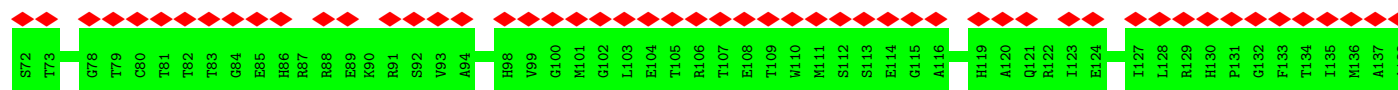
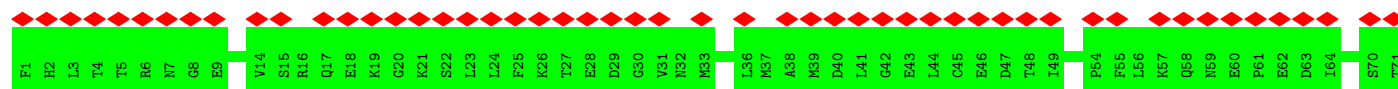
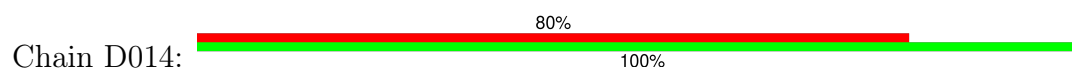
• Molecule 2: Protein prM



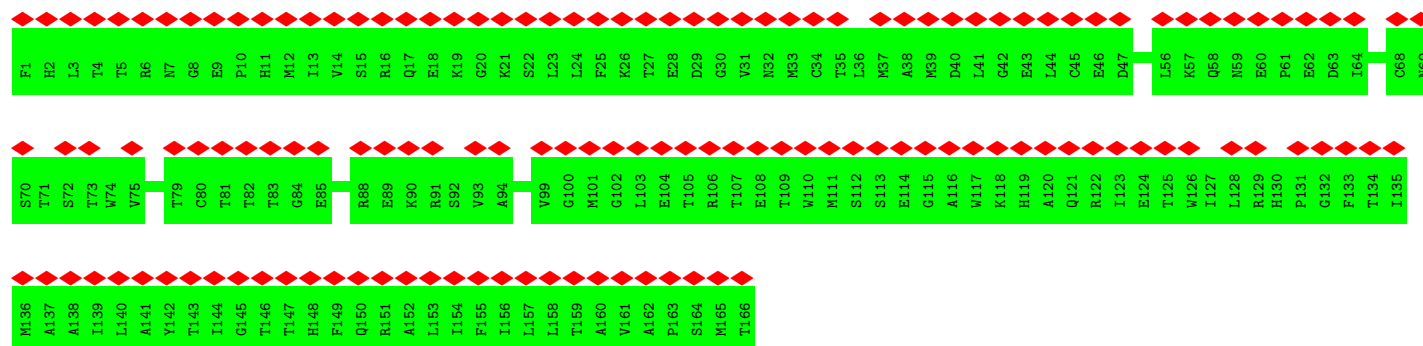
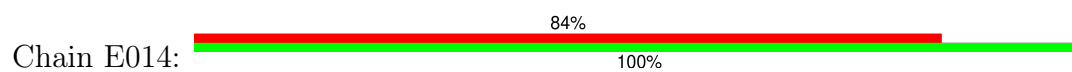
• Molecule 2: Protein prM



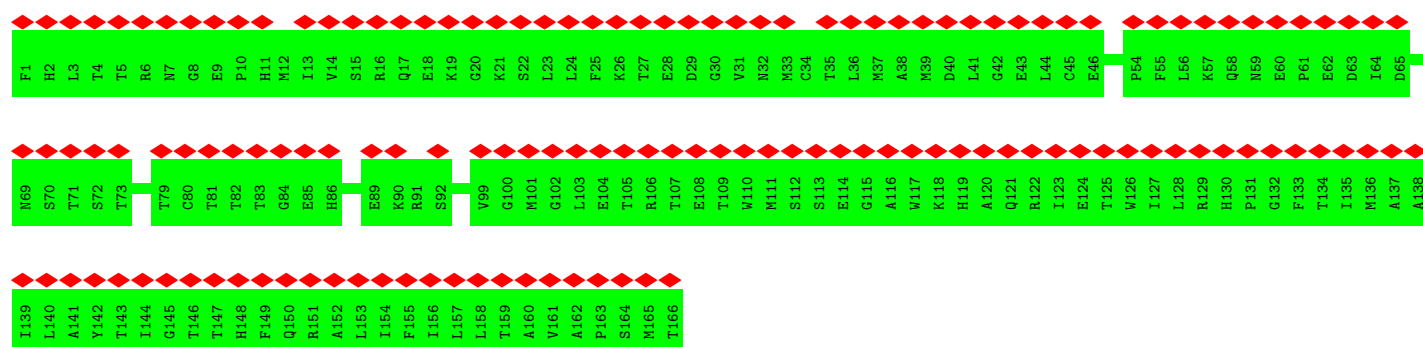
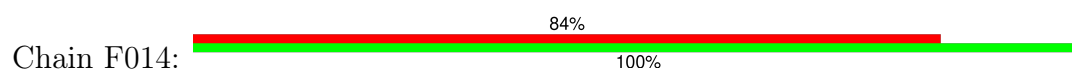
• Molecule 2: Protein prM



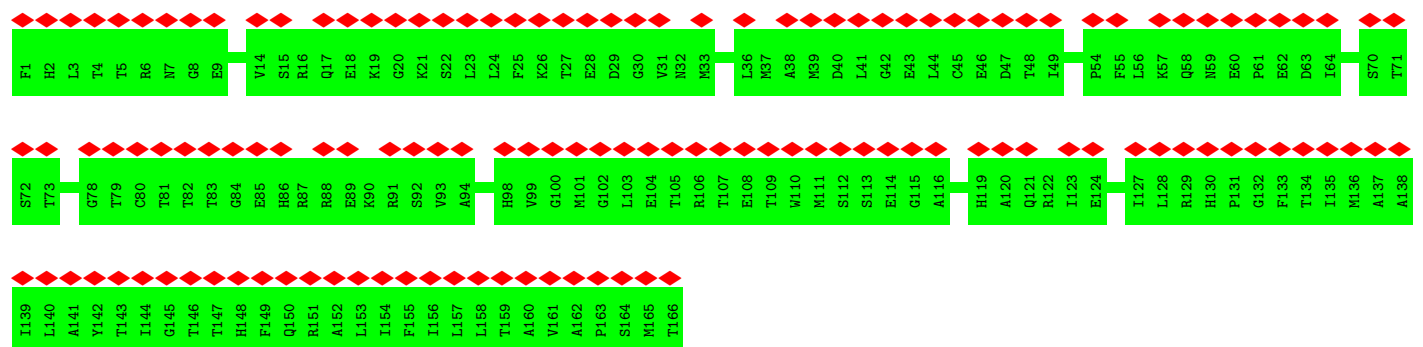
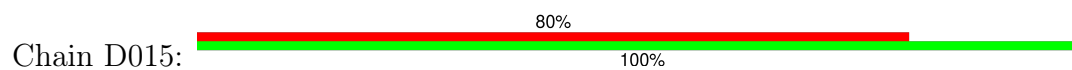
• Molecule 2: Protein prM



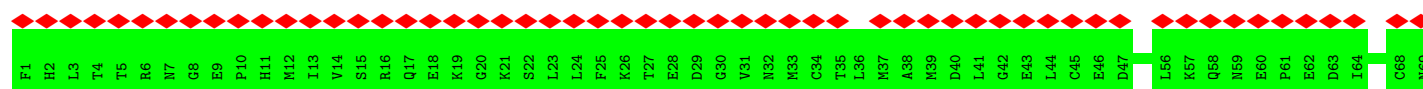
• Molecule 2: Protein prM

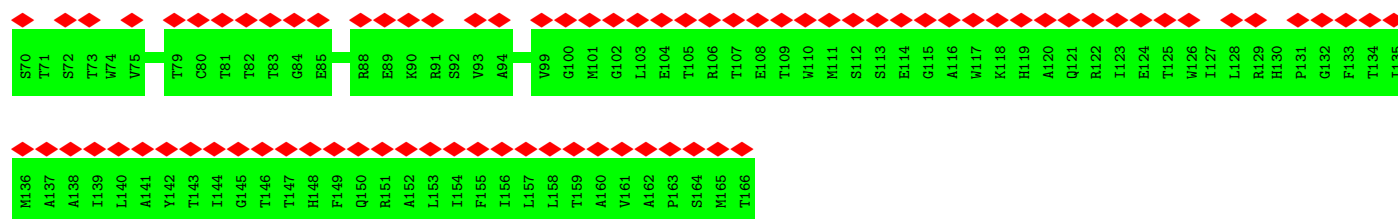


• Molecule 2: Protein prM

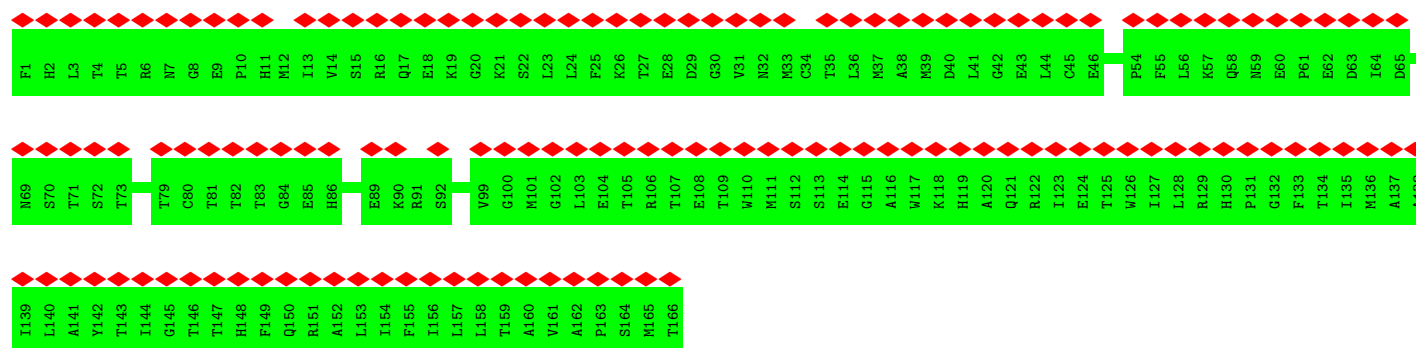
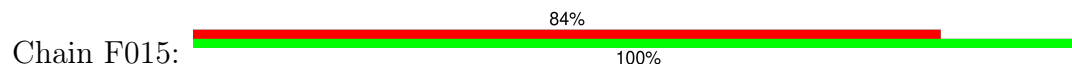


• Molecule 2: Protein prM

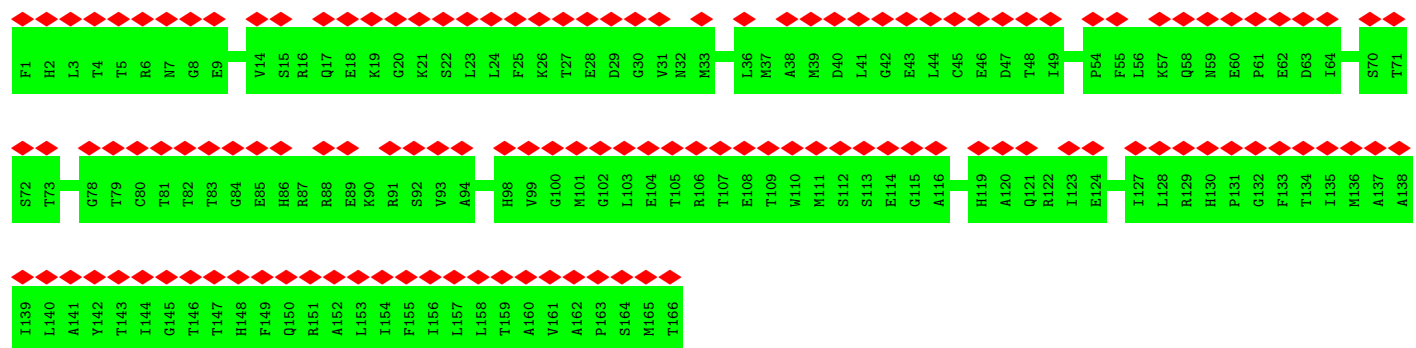
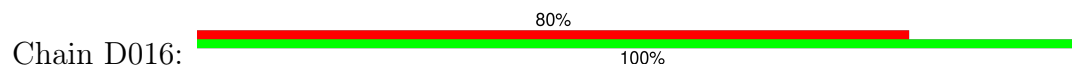




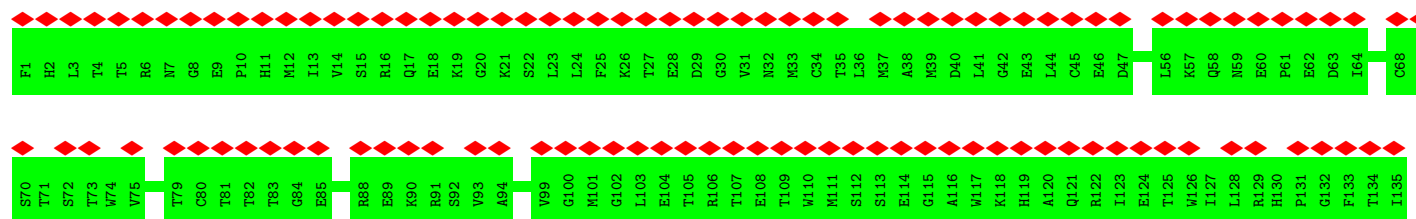
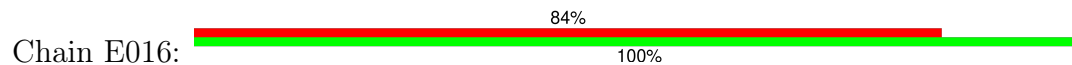
• Molecule 2: Protein prM

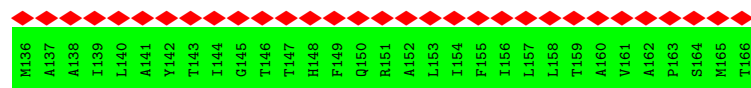


• Molecule 2: Protein prM

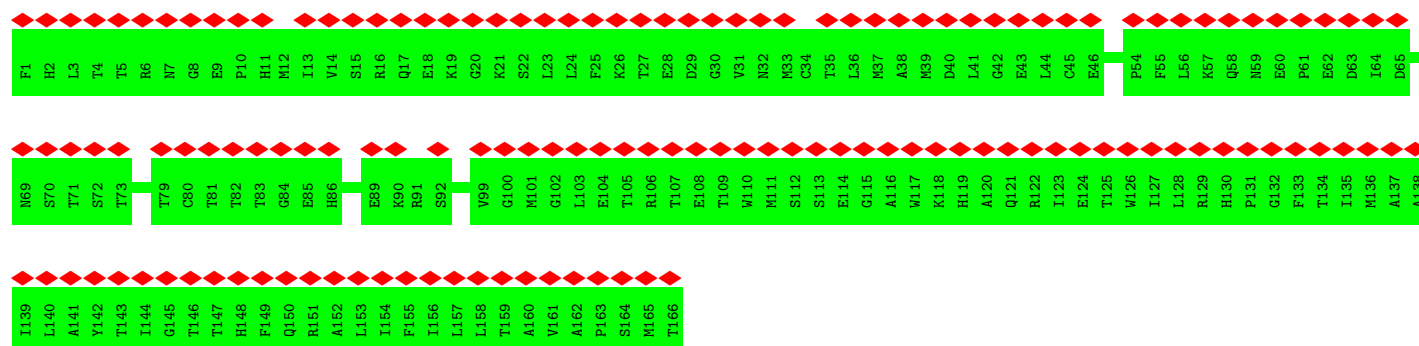
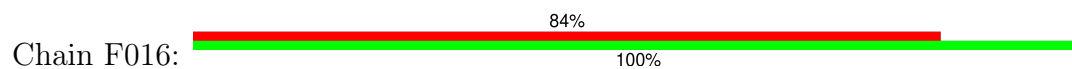


• Molecule 2: Protein prM

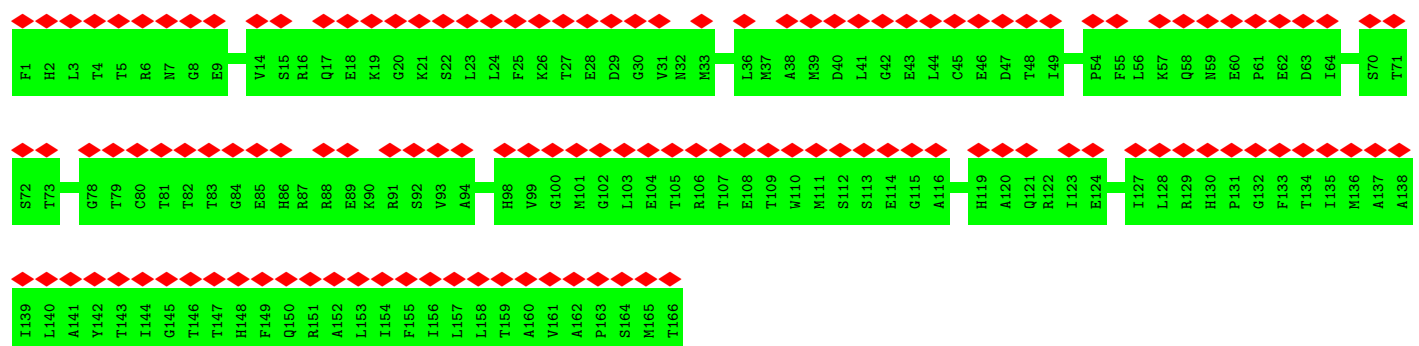
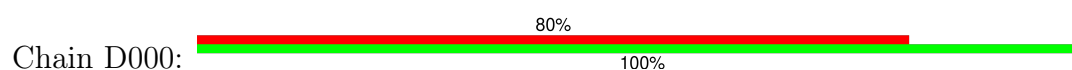




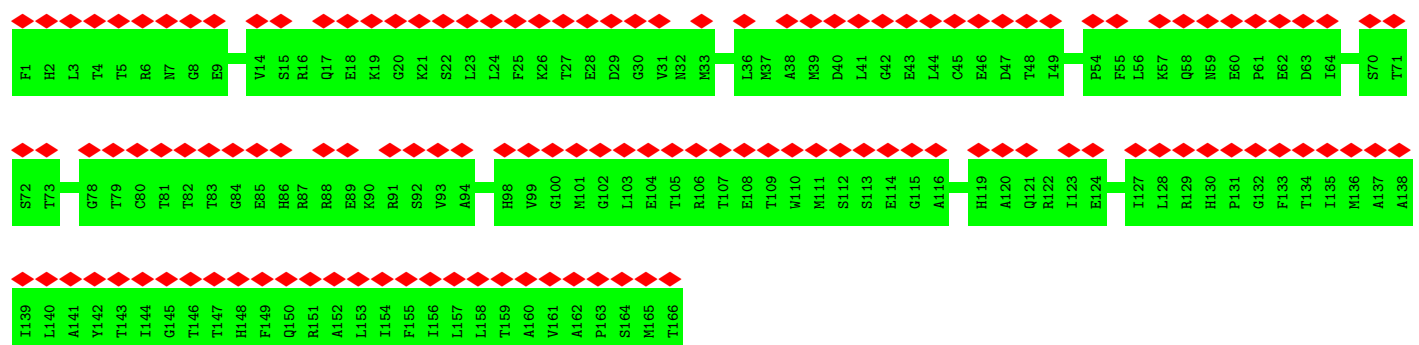
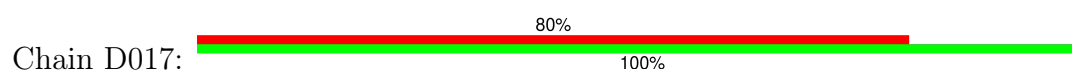
- Molecule 2: Protein prM



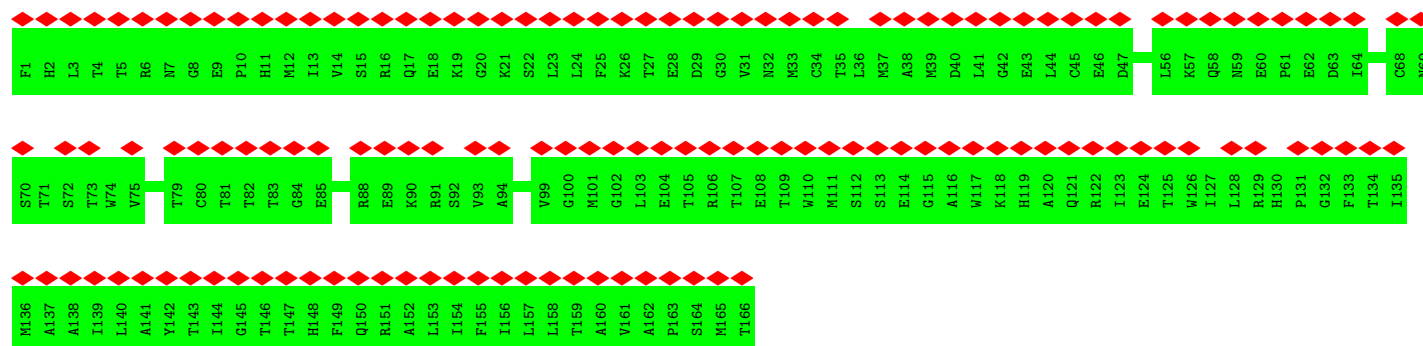
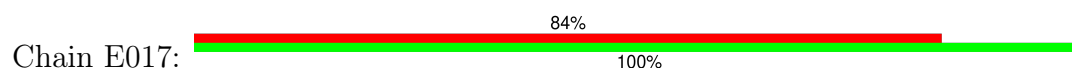
- Molecule 2: Protein prM



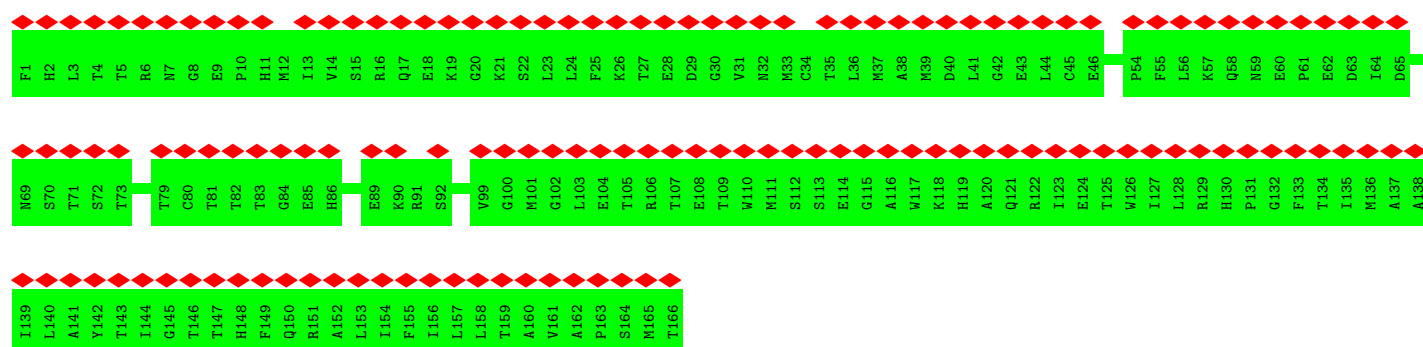
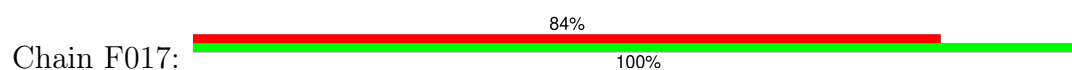
- Molecule 2: Protein prM



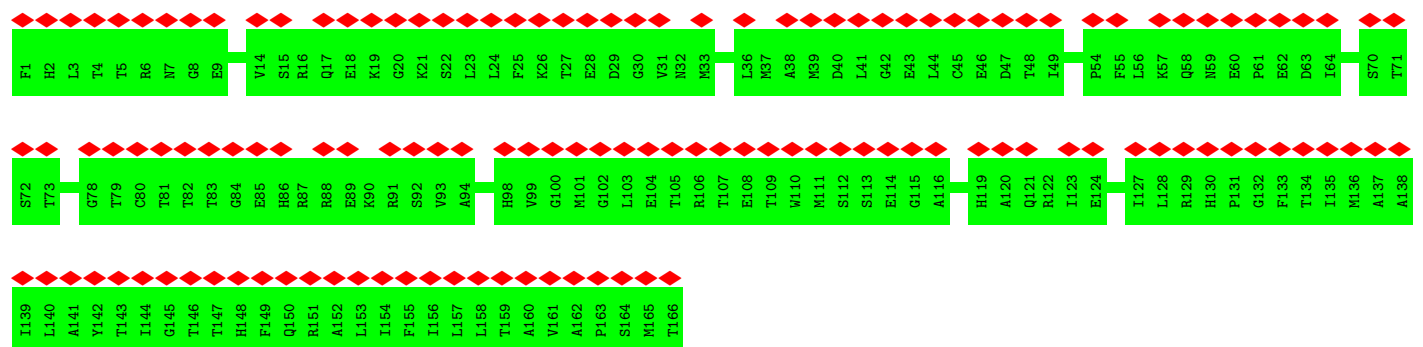
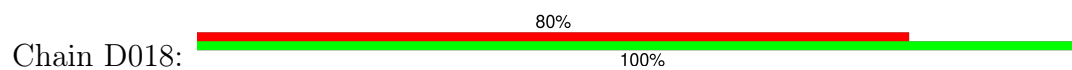
- Molecule 2: Protein prM



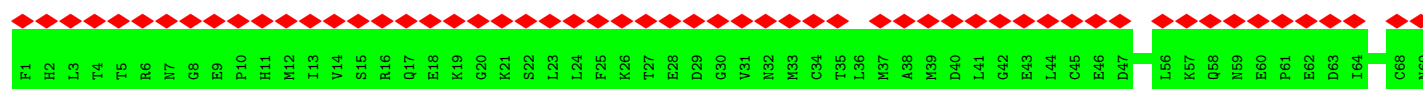
• Molecule 2: Protein prM

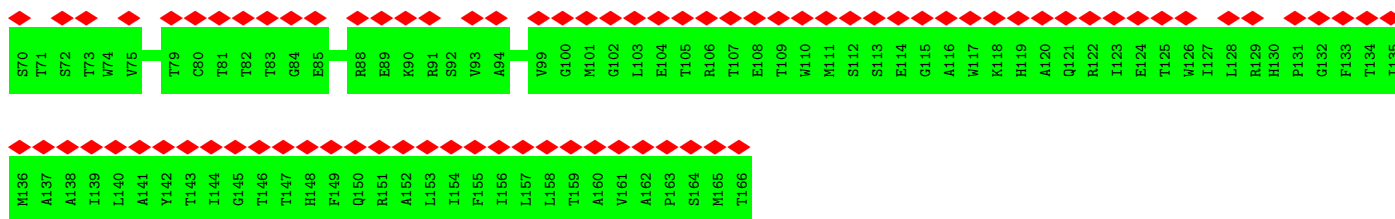


• Molecule 2: Protein prM

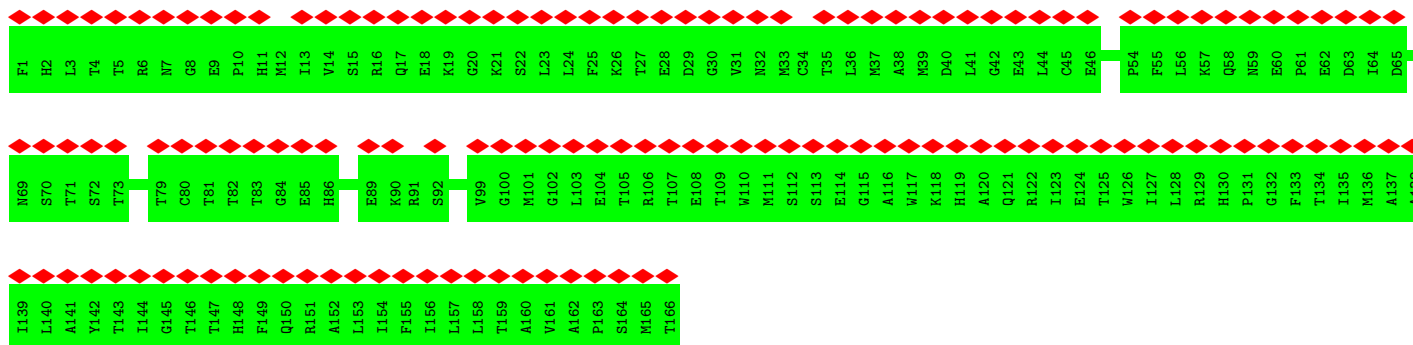
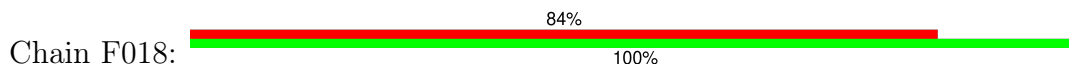


• Molecule 2: Protein prM

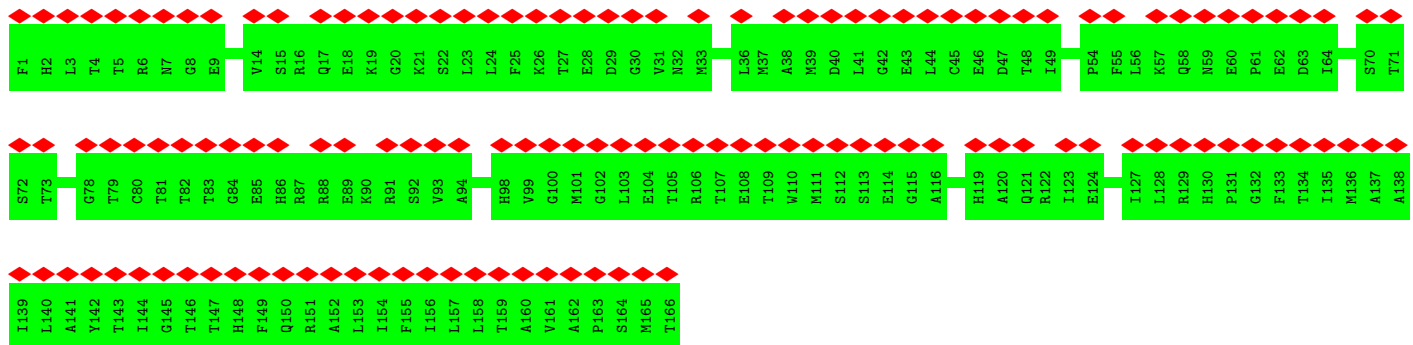
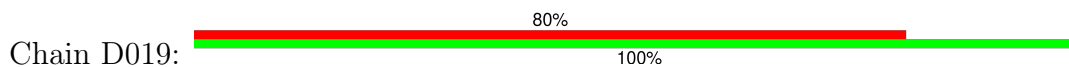




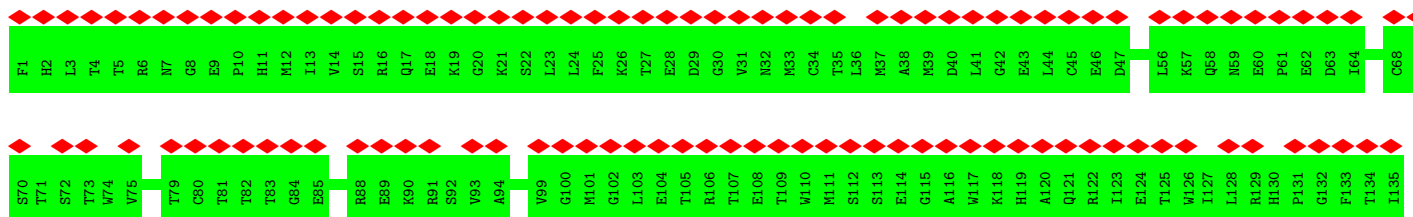
• Molecule 2: Protein prM



• Molecule 2: Protein prM

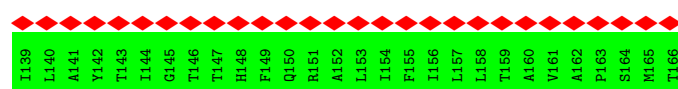
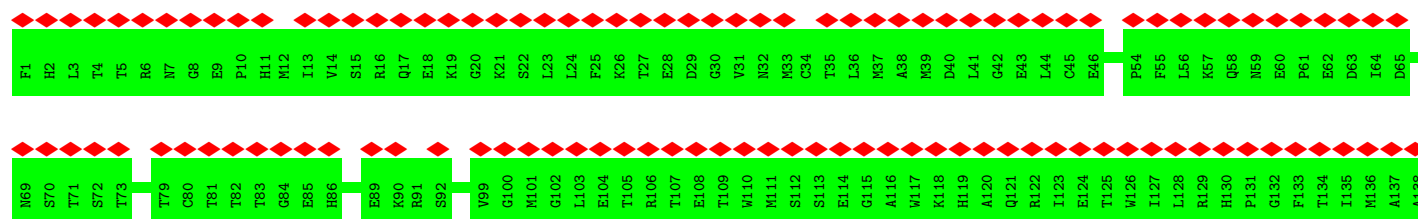
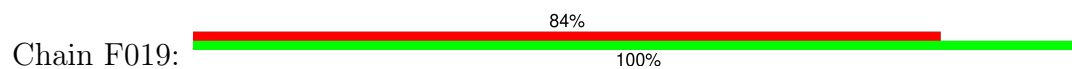


• Molecule 2: Protein prM

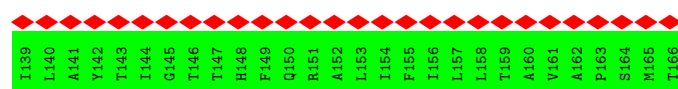
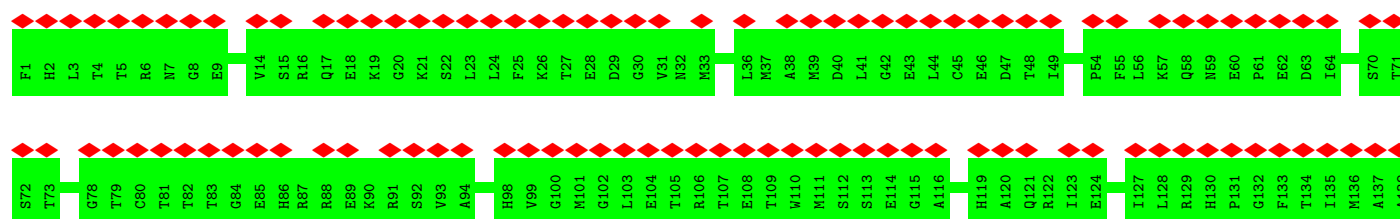
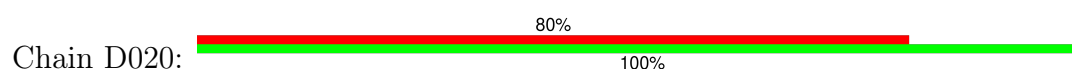




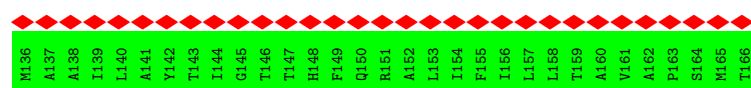
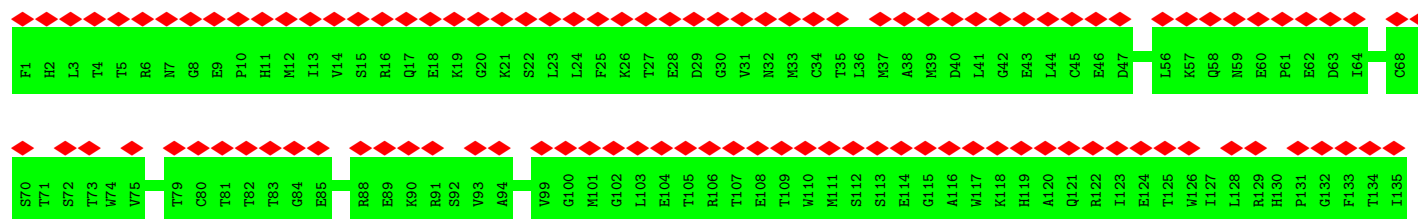
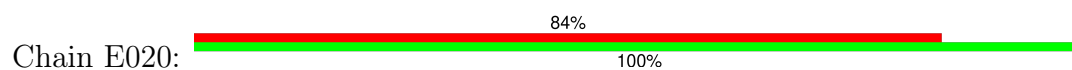
- Molecule 2: Protein prM



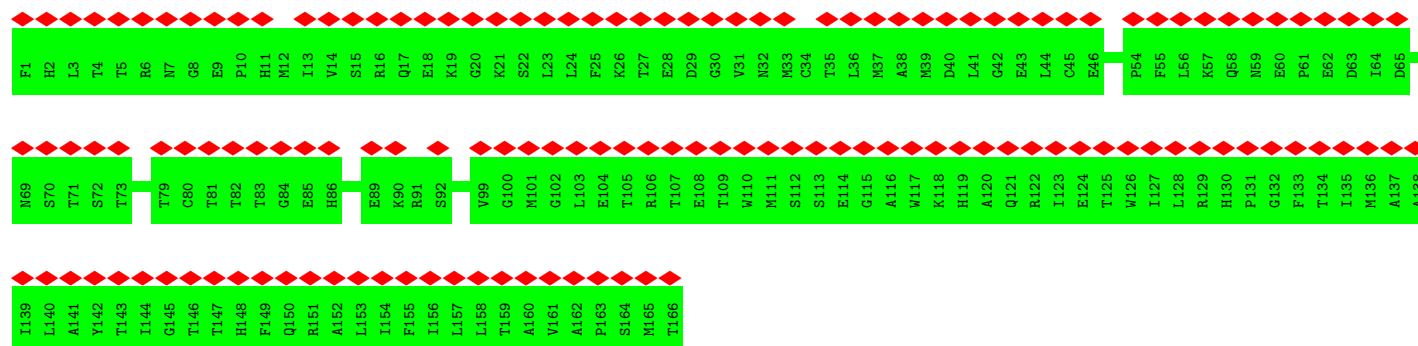
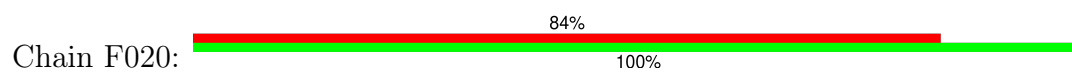
- Molecule 2: Protein prM



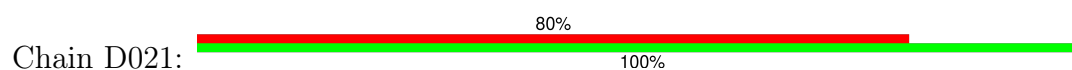
- Molecule 2: Protein prM



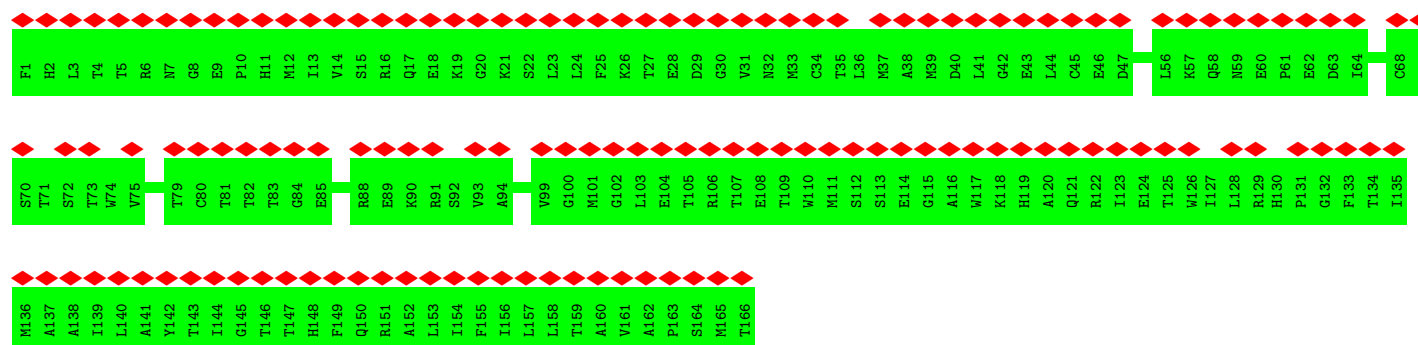
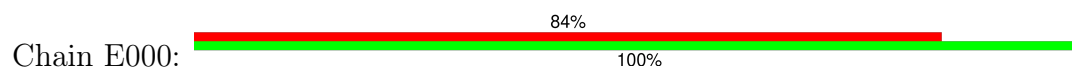
- Molecule 2: Protein prM



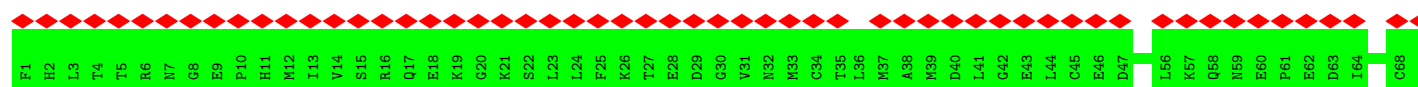
• Molecule 2: Protein prM

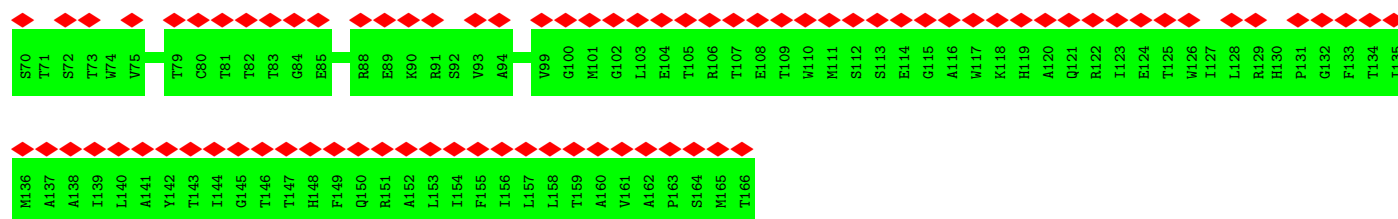


• Molecule 2: Protein prM

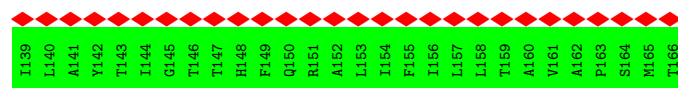
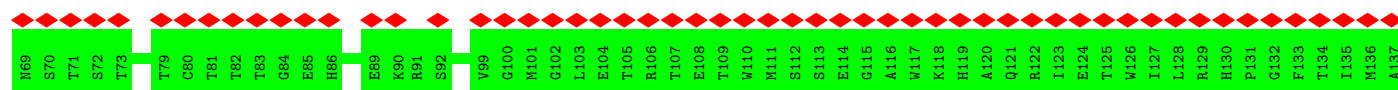
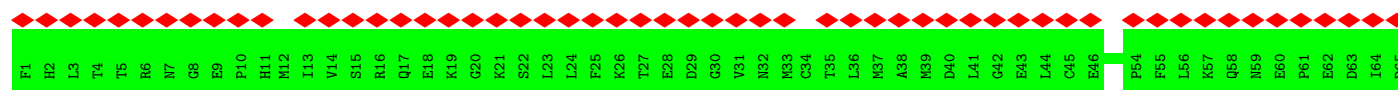
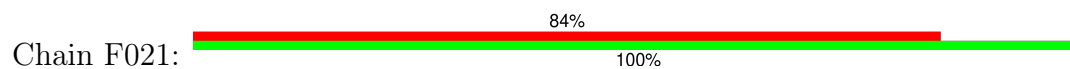


• Molecule 2: Protein prM

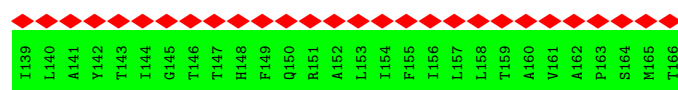
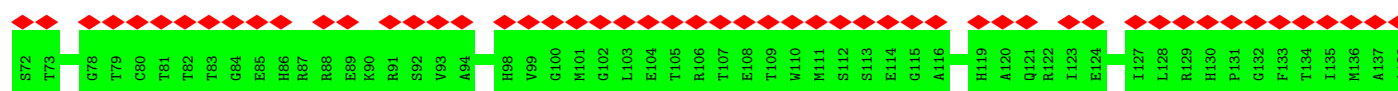
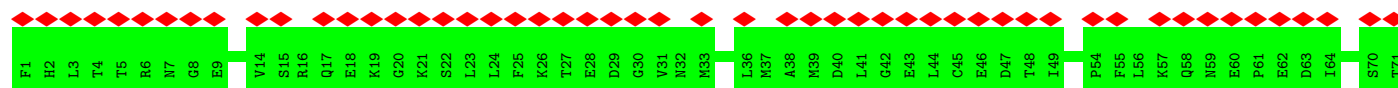
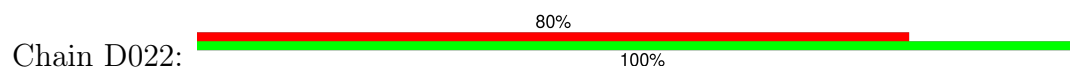




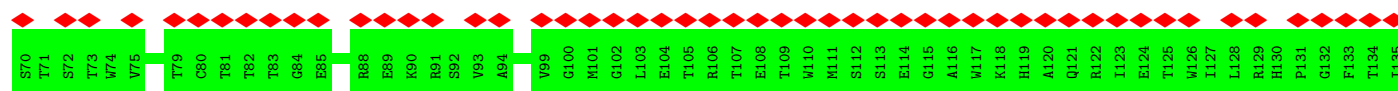
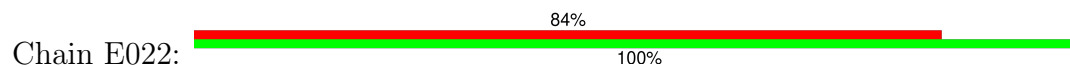
• Molecule 2: Protein prM



• Molecule 2: Protein prM

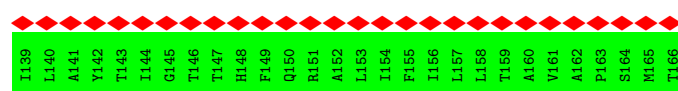
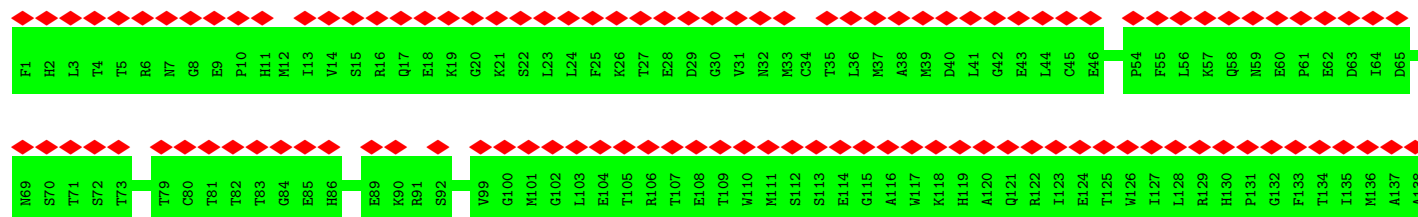
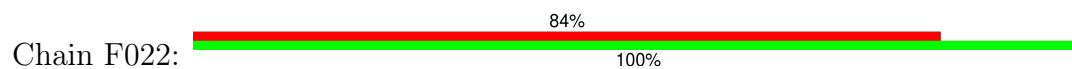


• Molecule 2: Protein prM

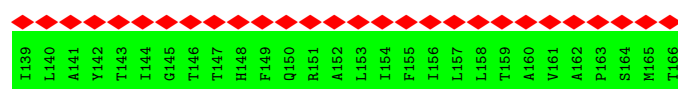
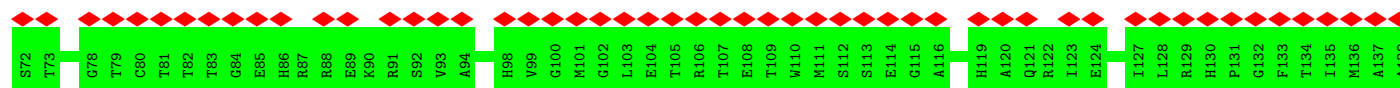
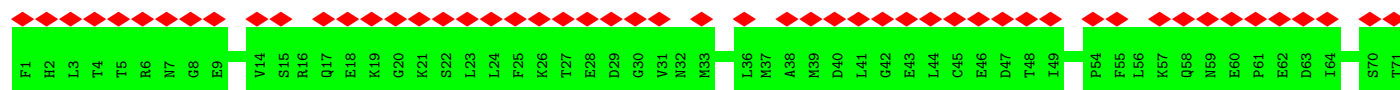
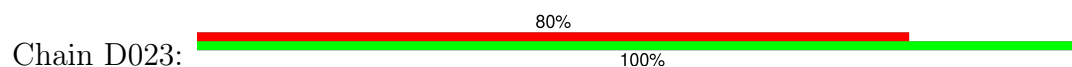




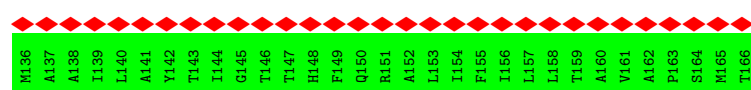
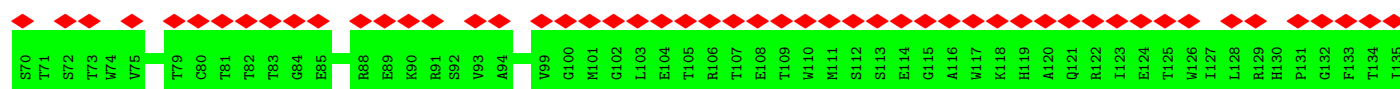
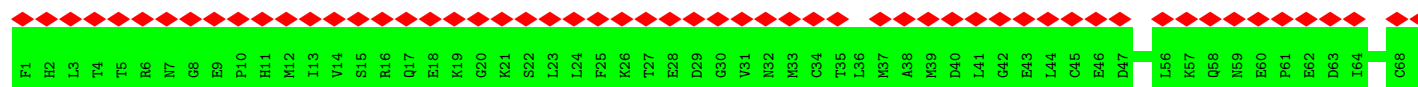
• Molecule 2: Protein prM



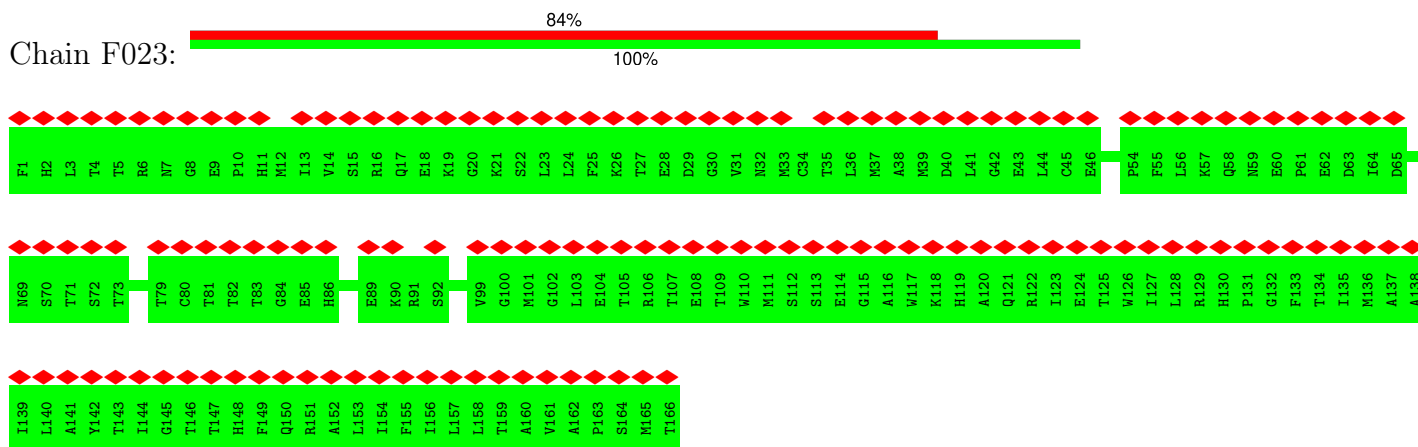
• Molecule 2: Protein prM



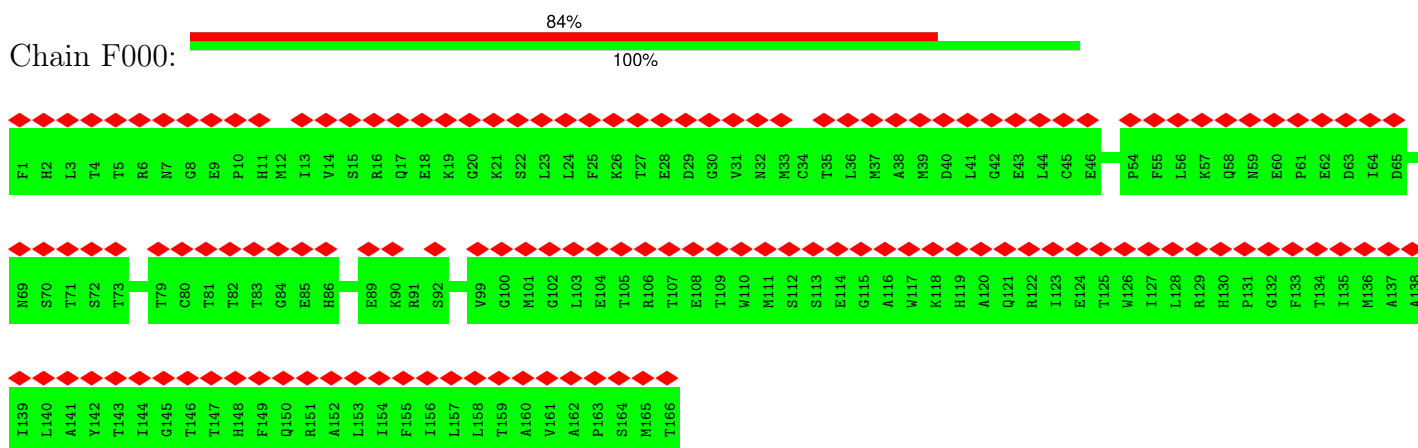
• Molecule 2: Protein prM



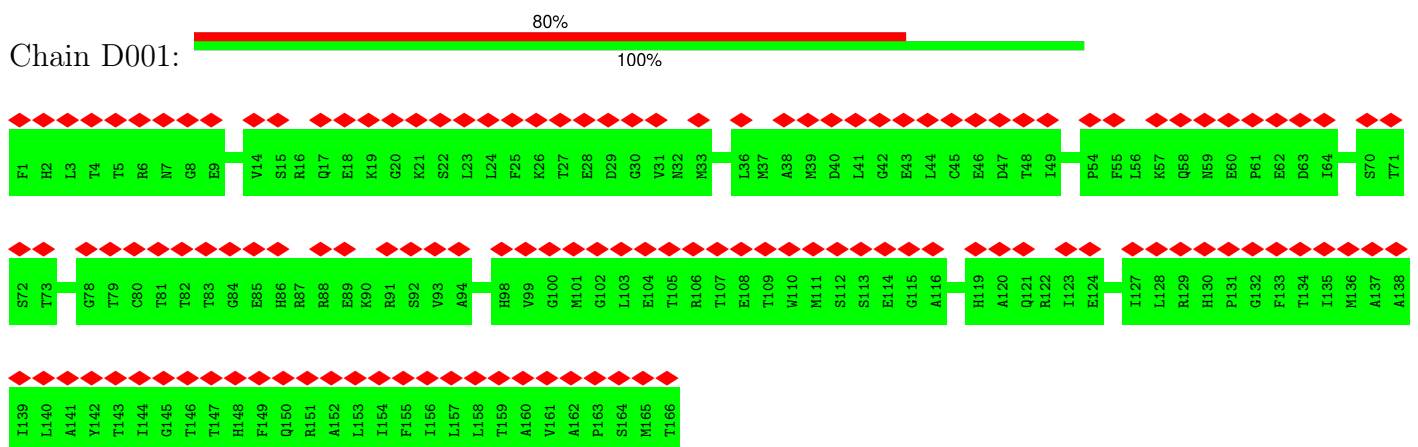
• Molecule 2: Protein prM



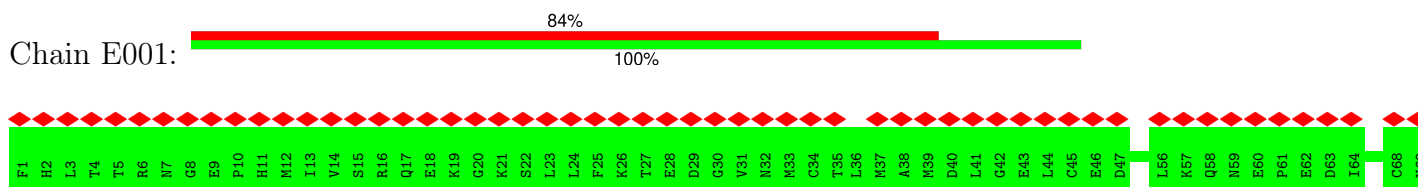
- Molecule 2: Protein prM

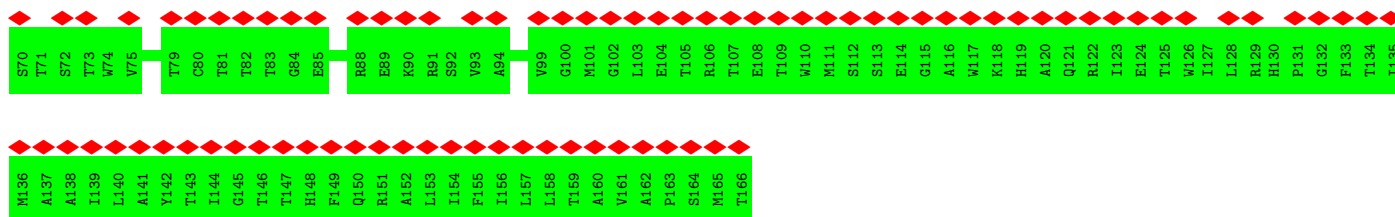


- Molecule 2: Protein prM

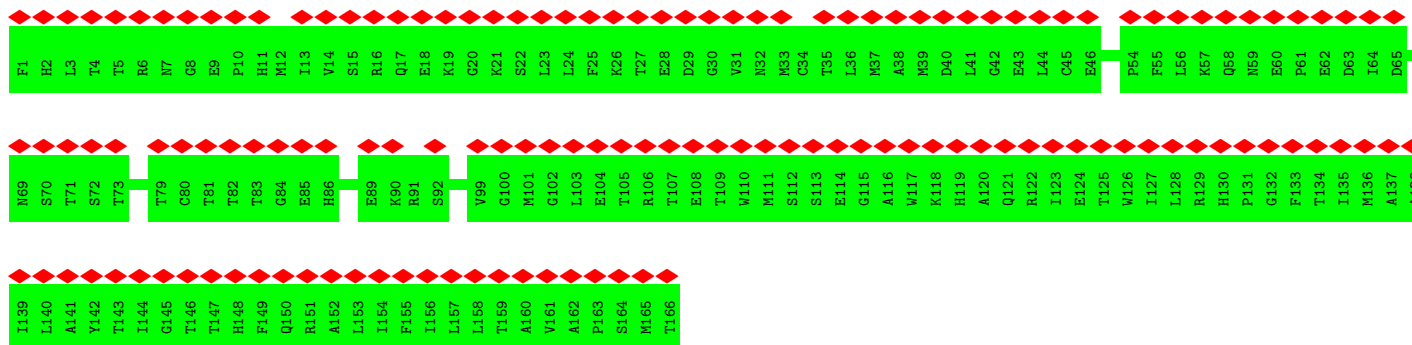
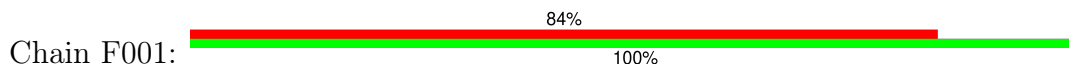


- Molecule 2: Protein prM

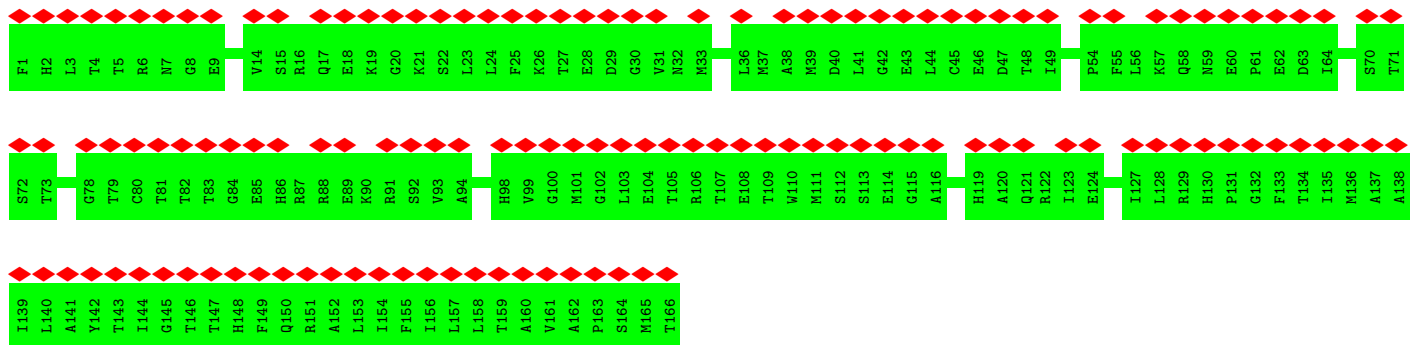
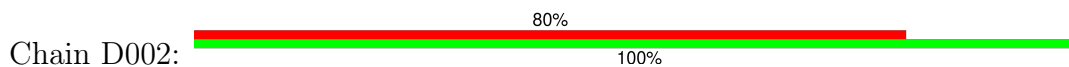




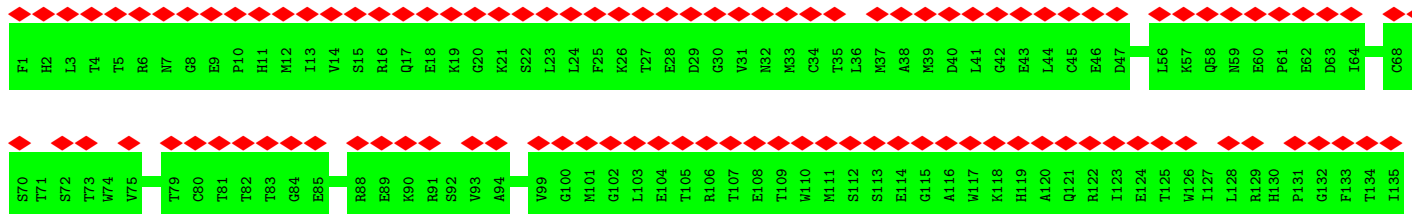
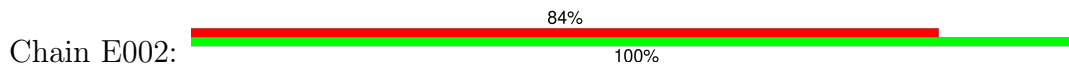
• Molecule 2: Protein prM



• Molecule 2: Protein prM

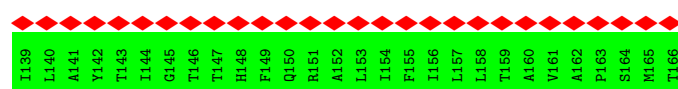
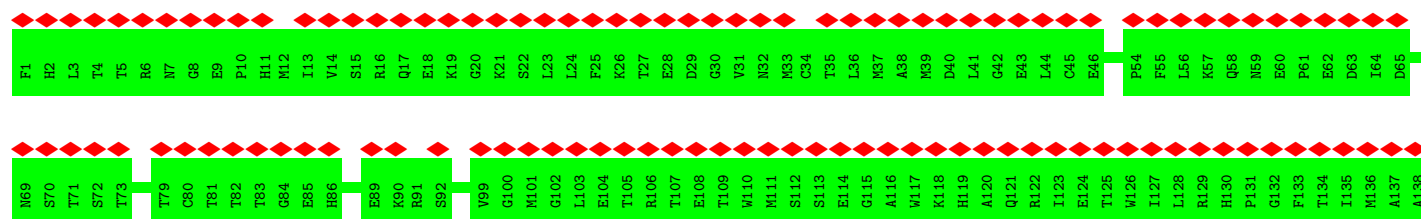
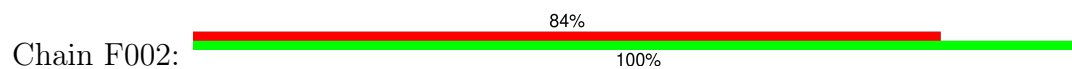


• Molecule 2: Protein prM

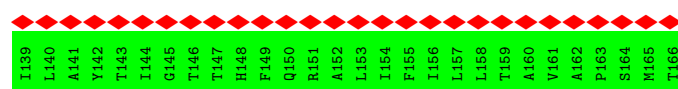
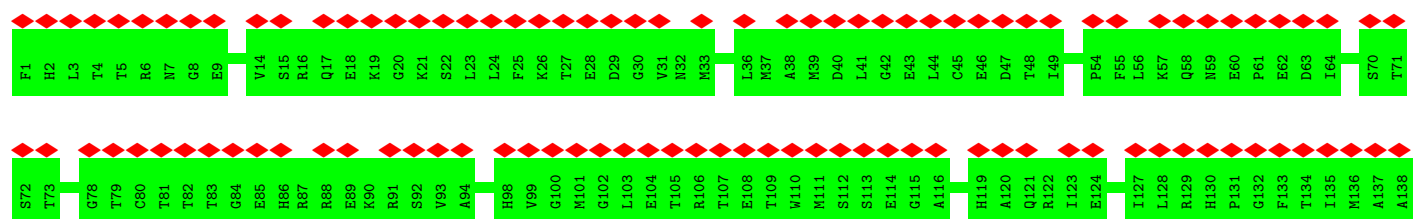
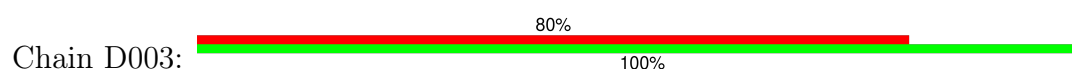




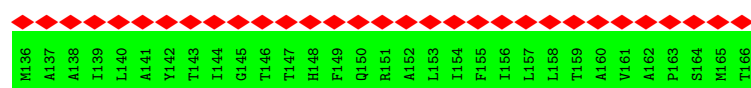
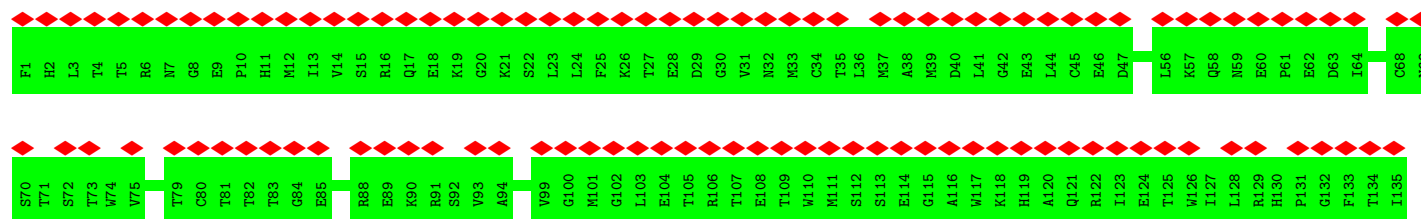
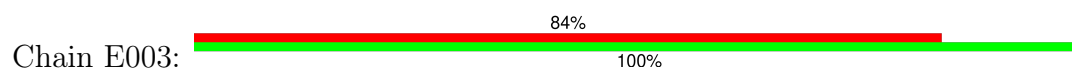
- Molecule 2: Protein prM



- Molecule 2: Protein prM



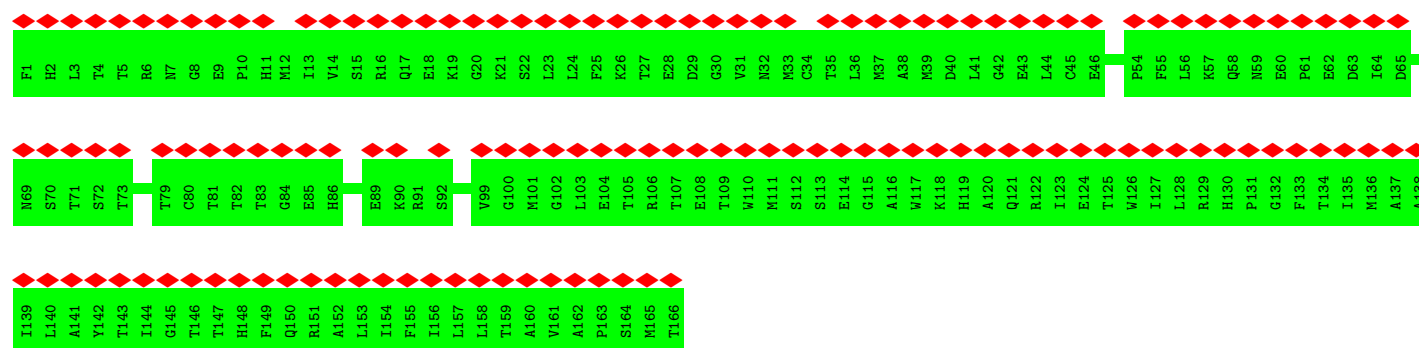
- Molecule 2: Protein prM



- Molecule 2: Protein prM

A horizontal bar chart with a red bar representing 84% and a green bar representing 100%. The red bar is labeled '84%' and the green bar is labeled '100%'.

Category	Value
Red Bar	84%
Green Bar	100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.3	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.006	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	629.76, 629.76, 629.76	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A000	495	0	0	0	0
1	A001	495	0	0	0	0
1	A002	495	0	0	0	0
1	A003	495	0	0	0	0
1	A004	495	0	0	0	0
1	A005	495	0	0	0	0
1	A006	495	0	0	0	0
1	A007	495	0	0	0	0
1	A008	495	0	0	0	0
1	A009	495	0	0	0	0
1	A010	495	0	0	0	0
1	A011	495	0	0	0	0
1	A012	495	0	0	0	0
1	A013	495	0	0	0	0
1	A014	495	0	0	0	0
1	A015	495	0	0	0	0
1	A016	495	0	0	0	0
1	A017	495	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A018	495	0	0	0	0
1	A019	495	0	0	0	0
1	A020	495	0	0	0	0
1	A021	495	0	0	0	0
1	A022	495	0	0	0	0
1	A023	495	0	0	0	0
1	B000	495	0	0	0	0
1	B001	495	0	0	0	0
1	B002	495	0	0	0	0
1	B003	495	0	0	0	0
1	B004	495	0	0	0	0
1	B005	495	0	0	0	0
1	B006	495	0	0	0	0
1	B007	495	0	0	0	0
1	B008	495	0	0	0	0
1	B009	495	0	0	0	0
1	B010	495	0	0	0	0
1	B011	495	0	0	0	0
1	B012	495	0	0	0	0
1	B013	495	0	0	0	0
1	B014	495	0	0	0	0
1	B015	495	0	0	0	0
1	B016	495	0	0	0	0
1	B017	495	0	0	0	0
1	B018	495	0	0	0	0
1	B019	495	0	0	0	0
1	B020	495	0	0	0	0
1	B021	495	0	0	0	0
1	B022	495	0	0	0	0
1	B023	495	0	0	0	0
1	C000	495	0	0	0	0
1	C001	495	0	0	0	0
1	C002	495	0	0	0	0
1	C003	495	0	0	0	0
1	C004	495	0	0	0	0
1	C005	495	0	0	0	0
1	C006	495	0	0	0	0
1	C007	495	0	0	0	0
1	C008	495	0	0	0	0
1	C009	495	0	0	0	0
1	C010	495	0	0	0	0
1	C011	495	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C012	495	0	0	0	0
1	C013	495	0	0	0	0
1	C014	495	0	0	0	0
1	C015	495	0	0	0	0
1	C016	495	0	0	0	0
1	C017	495	0	0	0	0
1	C018	495	0	0	0	0
1	C019	495	0	0	0	0
1	C020	495	0	0	0	0
1	C021	495	0	0	0	0
1	C022	495	0	0	0	0
1	C023	495	0	0	0	0
2	D000	166	0	0	0	0
2	D001	166	0	0	0	0
2	D002	166	0	0	0	0
2	D003	166	0	0	0	0
2	D004	166	0	0	0	0
2	D005	166	0	0	0	0
2	D006	166	0	0	0	0
2	D007	166	0	0	0	0
2	D008	166	0	0	0	0
2	D009	166	0	0	0	0
2	D010	166	0	0	0	0
2	D011	166	0	0	0	0
2	D012	166	0	0	0	0
2	D013	166	0	0	0	0
2	D014	166	0	0	0	0
2	D015	166	0	0	0	0
2	D016	166	0	0	0	0
2	D017	166	0	0	0	0
2	D018	166	0	0	0	0
2	D019	166	0	0	0	0
2	D020	166	0	0	0	0
2	D021	166	0	0	0	0
2	D022	166	0	0	0	0
2	D023	166	0	0	0	0
2	E000	166	0	0	0	0
2	E001	166	0	0	0	0
2	E002	166	0	0	0	0
2	E003	166	0	0	0	0
2	E004	166	0	0	0	0
2	E005	166	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E006	166	0	0	0	0
2	E007	166	0	0	0	0
2	E008	166	0	0	0	0
2	E009	166	0	0	0	0
2	E010	166	0	0	0	0
2	E011	166	0	0	0	0
2	E012	166	0	0	0	0
2	E013	166	0	0	0	0
2	E014	166	0	0	0	0
2	E015	166	0	0	0	0
2	E016	166	0	0	0	0
2	E017	166	0	0	0	0
2	E018	166	0	0	0	0
2	E019	166	0	0	0	0
2	E020	166	0	0	0	0
2	E021	166	0	0	0	0
2	E022	166	0	0	0	0
2	E023	166	0	0	0	0
2	F000	166	0	0	0	0
2	F001	166	0	0	0	0
2	F002	166	0	0	0	0
2	F003	166	0	0	0	0
2	F004	166	0	0	0	0
2	F005	166	0	0	0	0
2	F006	166	0	0	0	0
2	F007	166	0	0	0	0
2	F008	166	0	0	0	0
2	F009	166	0	0	0	0
2	F010	166	0	0	0	0
2	F011	166	0	0	0	0
2	F012	166	0	0	0	0
2	F013	166	0	0	0	0
2	F014	166	0	0	0	0
2	F015	166	0	0	0	0
2	F016	166	0	0	0	0
2	F017	166	0	0	0	0
2	F018	166	0	0	0	0
2	F019	166	0	0	0	0
2	F020	166	0	0	0	0
2	F021	166	0	0	0	0
2	F022	166	0	0	0	0
2	F023	166	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	47592	0	0	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

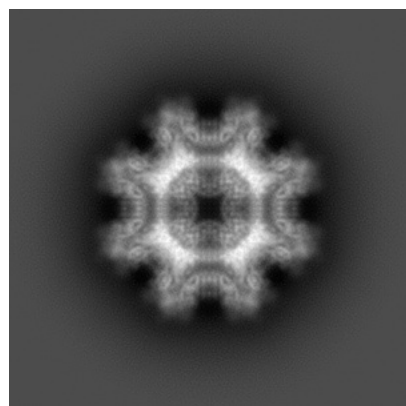
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47083. These allow visual inspection of the internal detail of the map and identification of artifacts.

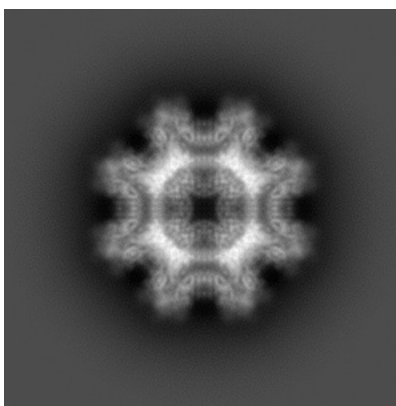
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

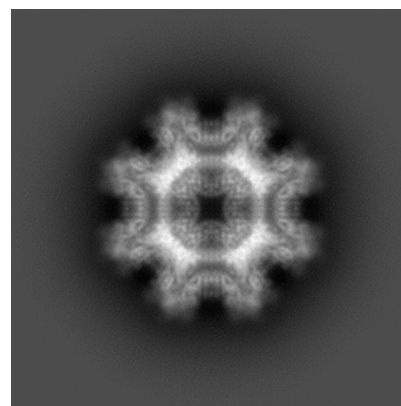
6.1.1 Primary map



X

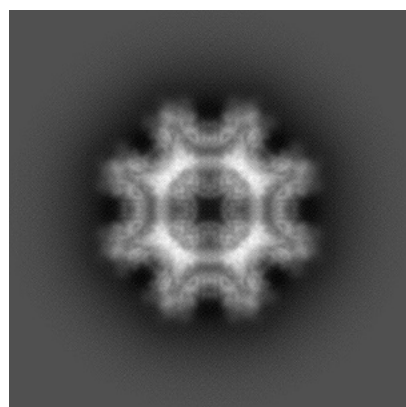


Y

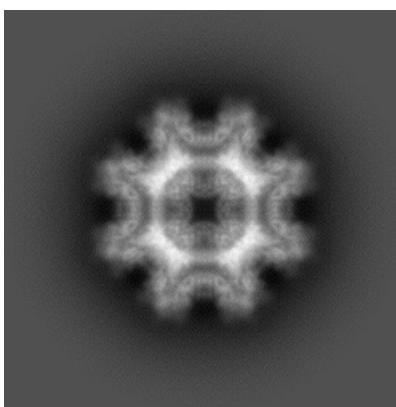


Z

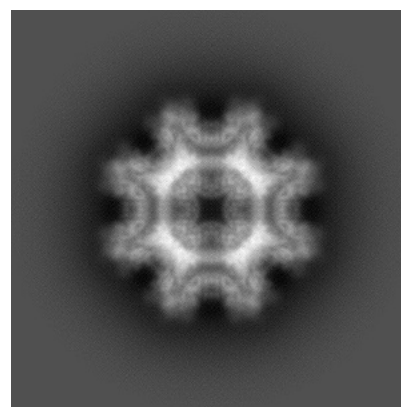
6.1.2 Raw map



X



Y

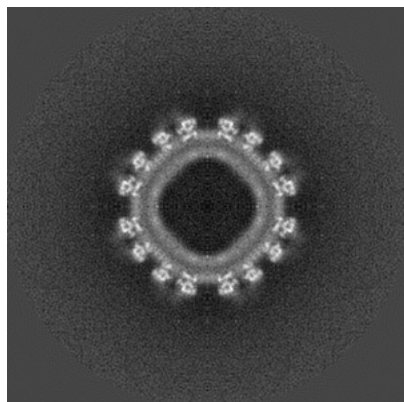


Z

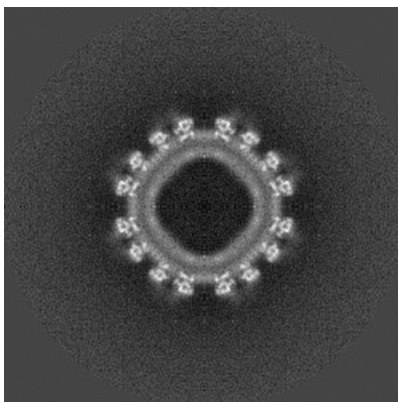
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

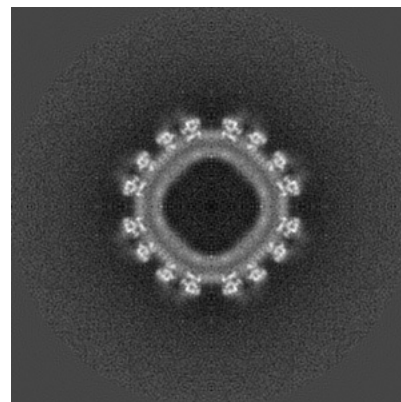
6.2.1 Primary map



X Index: 256

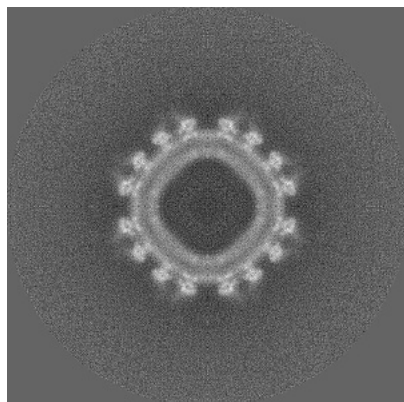


Y Index: 256

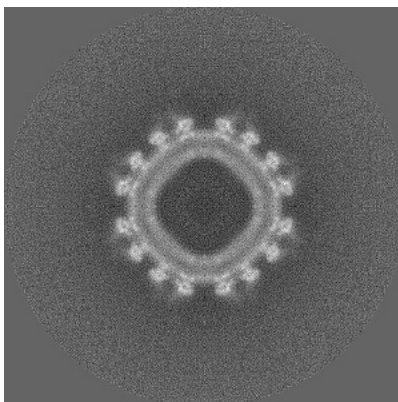


Z Index: 256

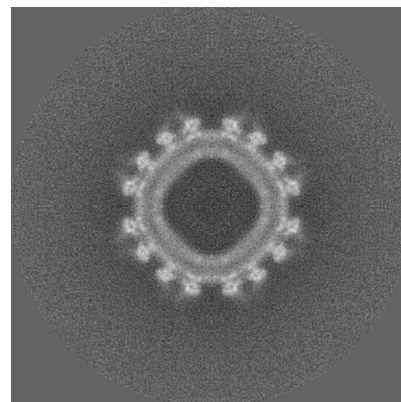
6.2.2 Raw map



X Index: 256



Y Index: 256

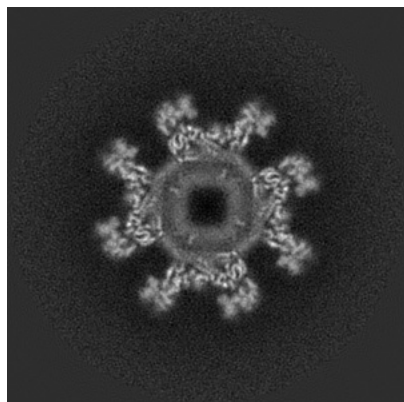


Z Index: 256

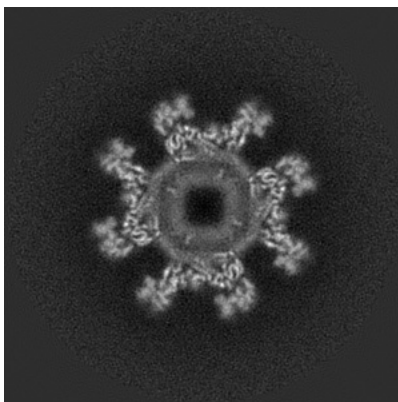
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

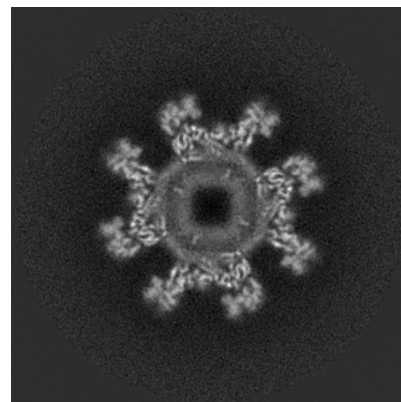
6.3.1 Primary map



X Index: 201

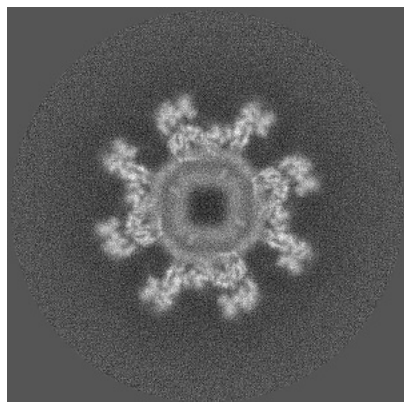


Y Index: 201

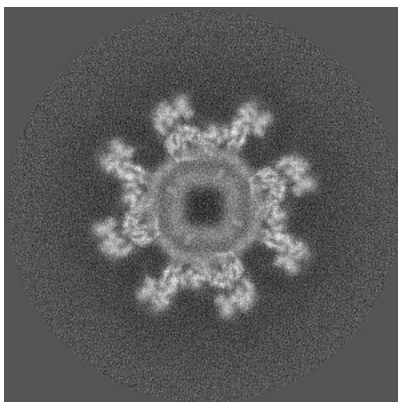


Z Index: 201

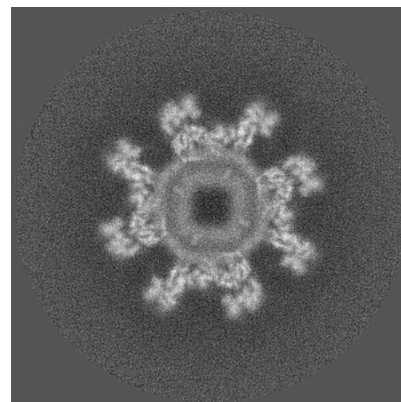
6.3.2 Raw map



X Index: 201



Y Index: 201

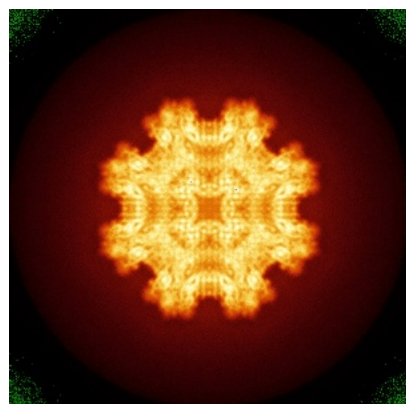


Z Index: 201

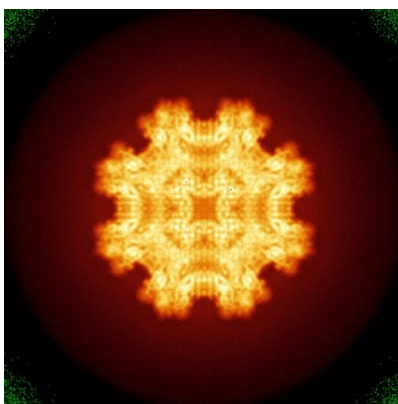
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

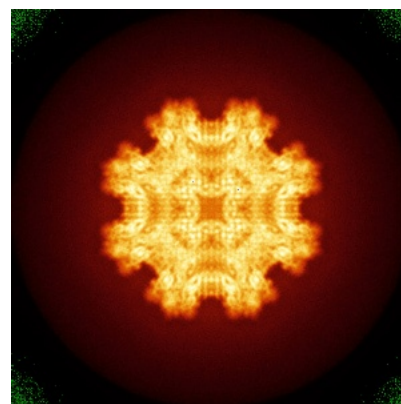
6.4.1 Primary map



X

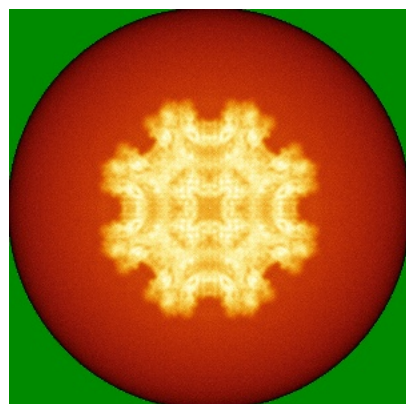


Y

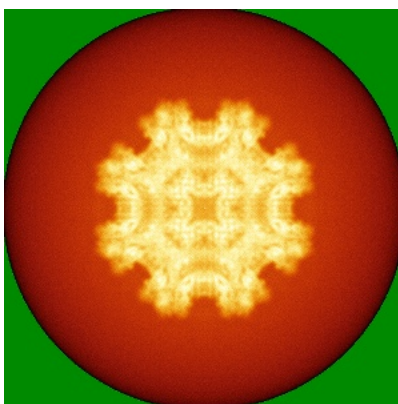


Z

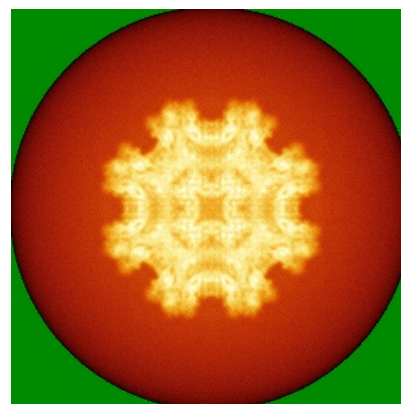
6.4.2 Raw map



X



Y

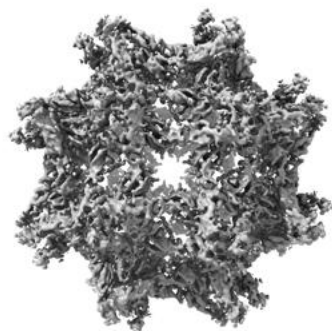


Z

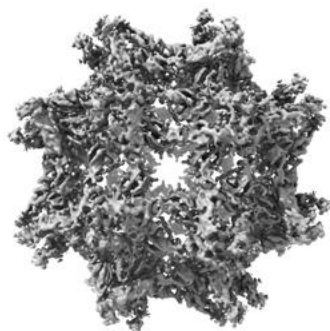
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

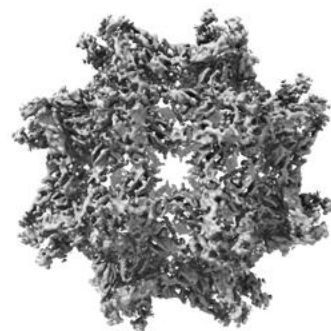
6.5.1 Primary map



X



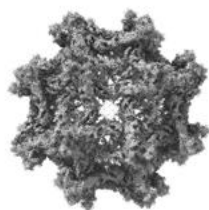
Y



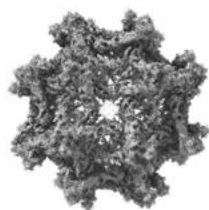
Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

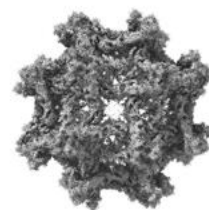
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

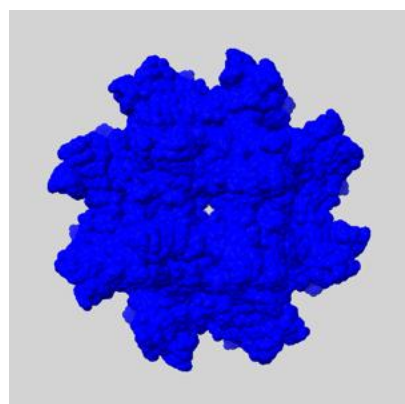
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

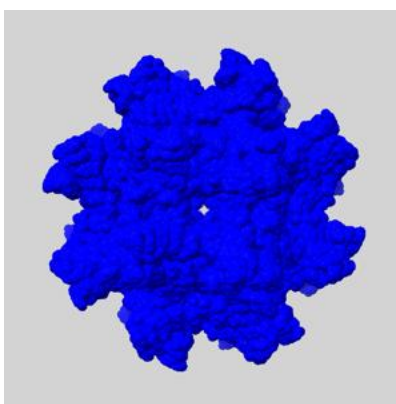
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

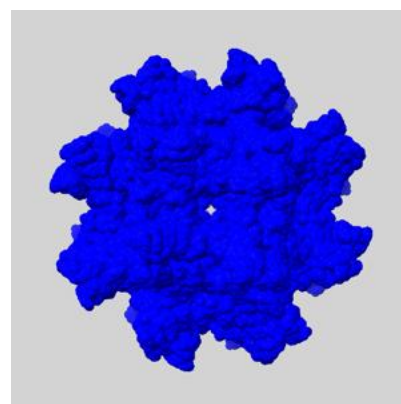
6.6.1 emd_47083_msk_1.map [i](#)



X



Y

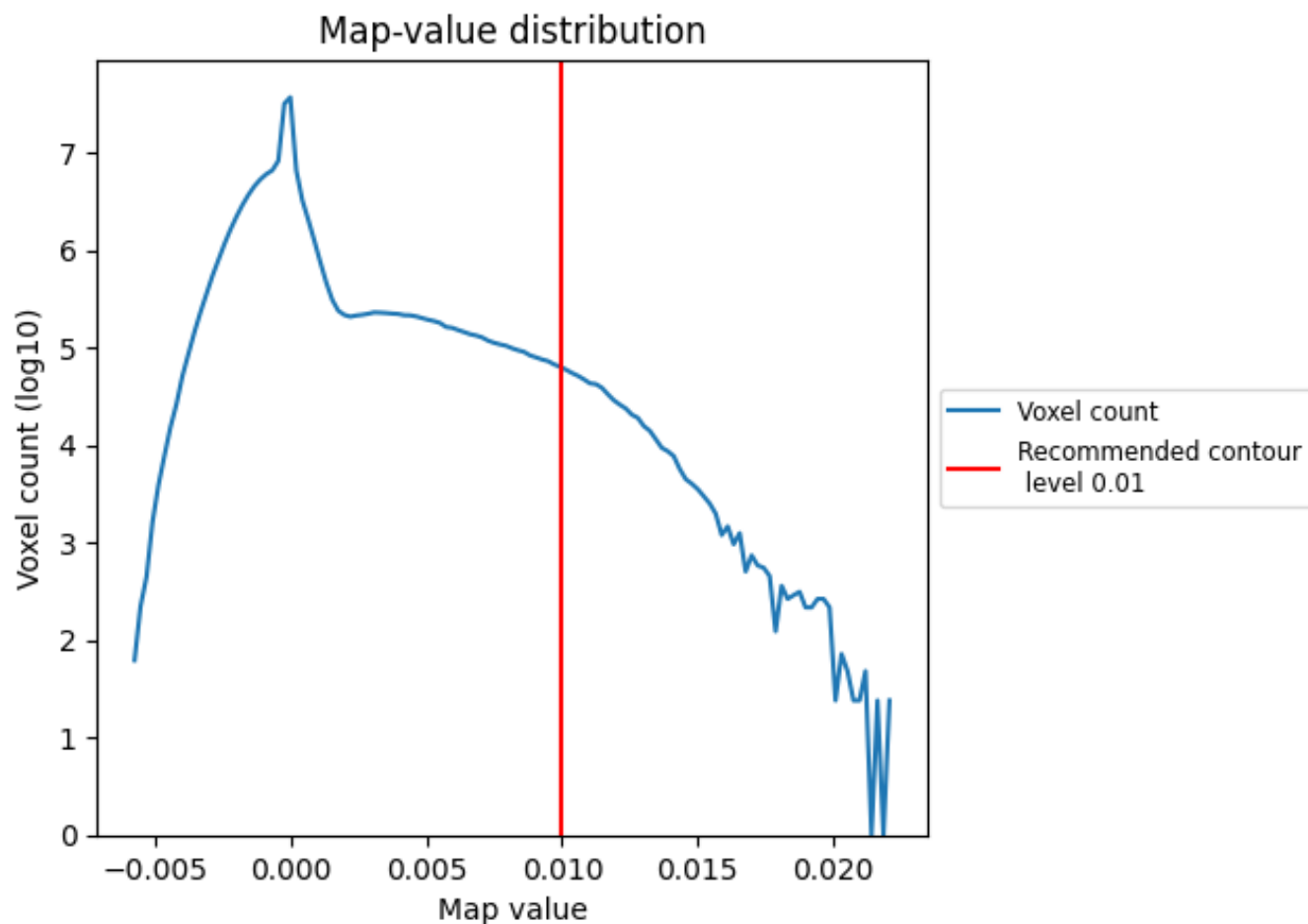


Z

7 Map analysis [i](#)

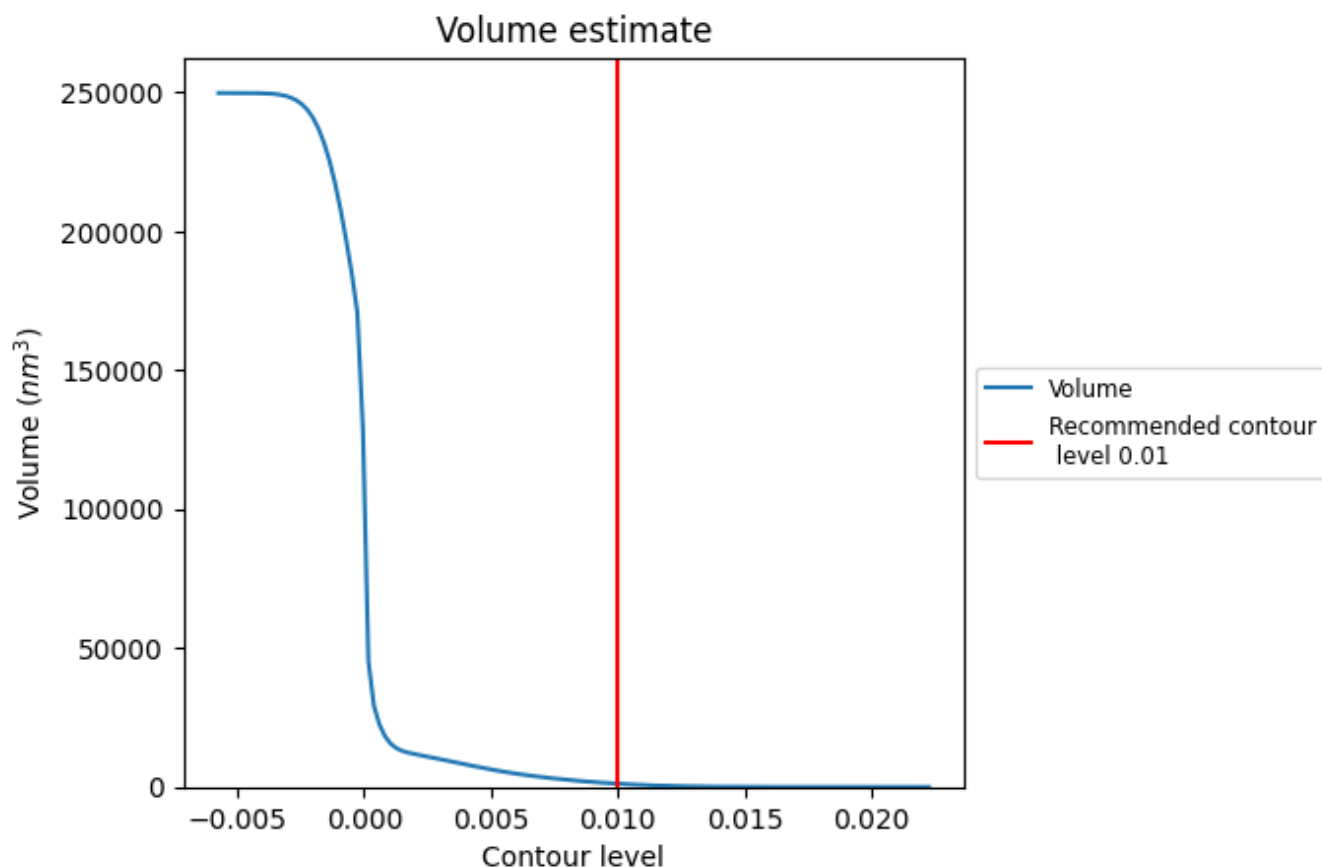
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

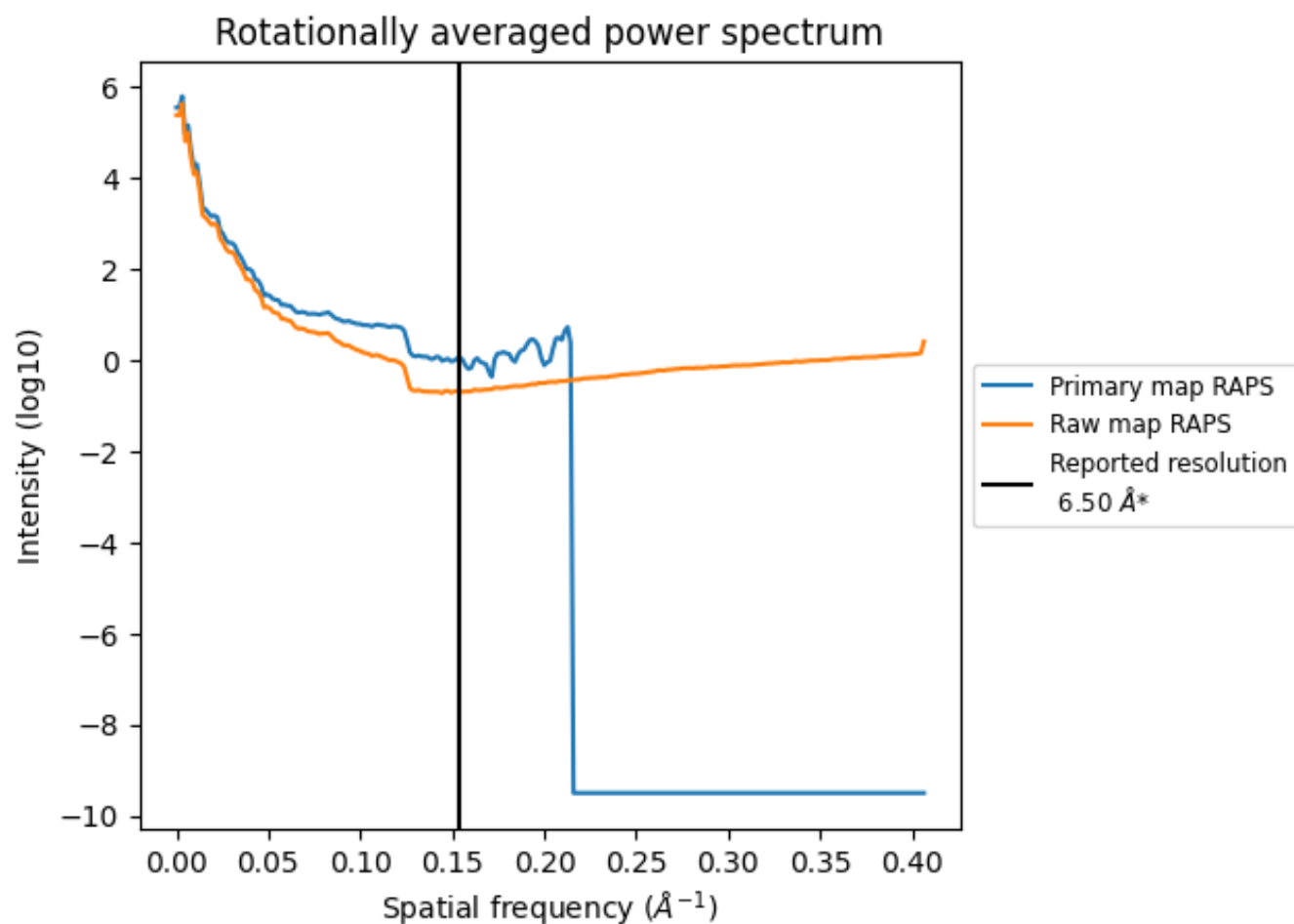
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1176 nm³; this corresponds to an approximate mass of 1062 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

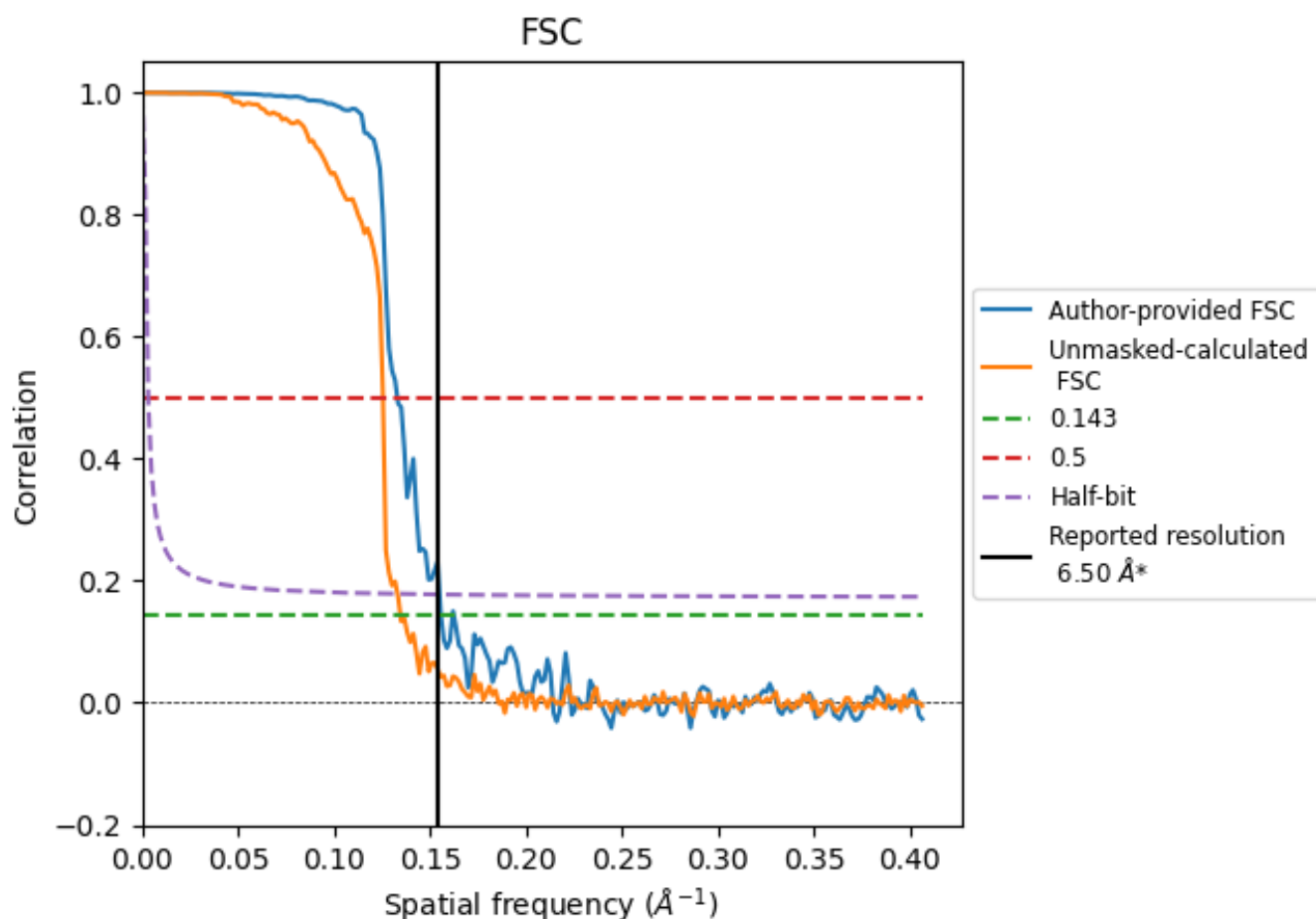


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.154 \AA^{-1}

8.2 Resolution estimates [i](#)

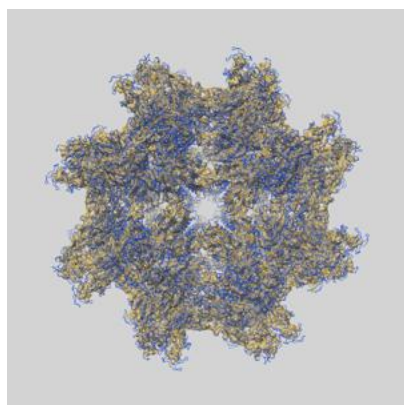
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.42	7.52	6.45
Unmasked-calculated*	7.43	7.97	7.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.43 differs from the reported value 6.5 by more than 10 %

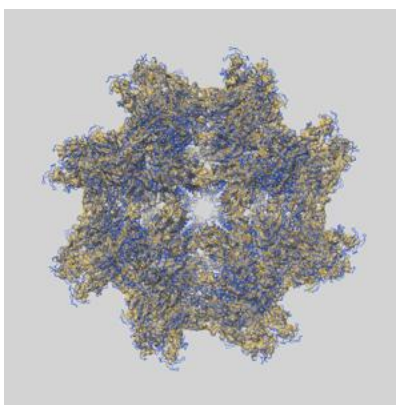
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47083 and PDB model 9DOG. Per-residue inclusion information can be found in section [3](#) on page [17](#).

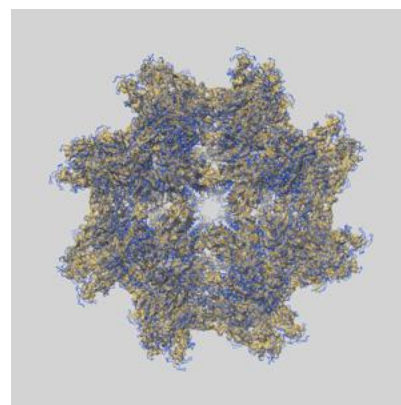
9.1 Map-model overlay [i](#)



X



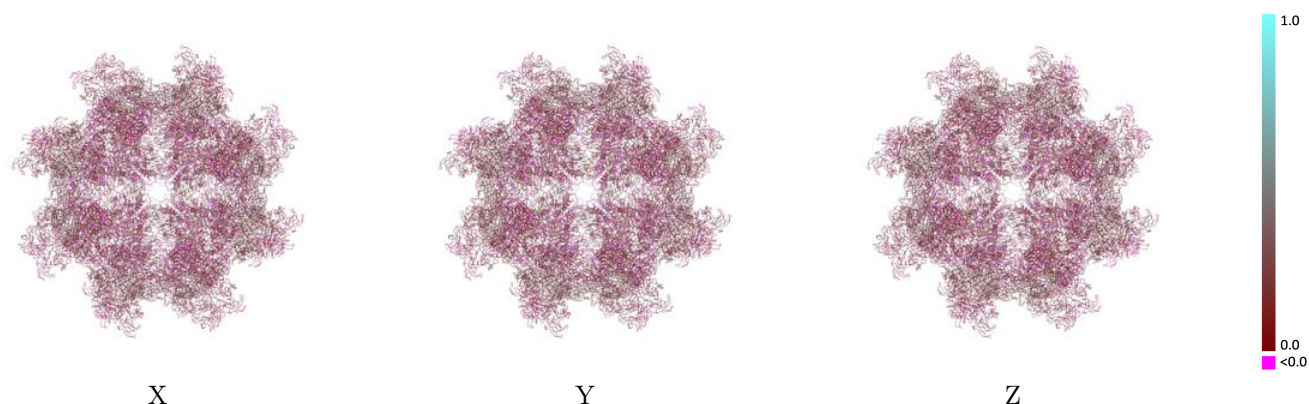
Y



Z

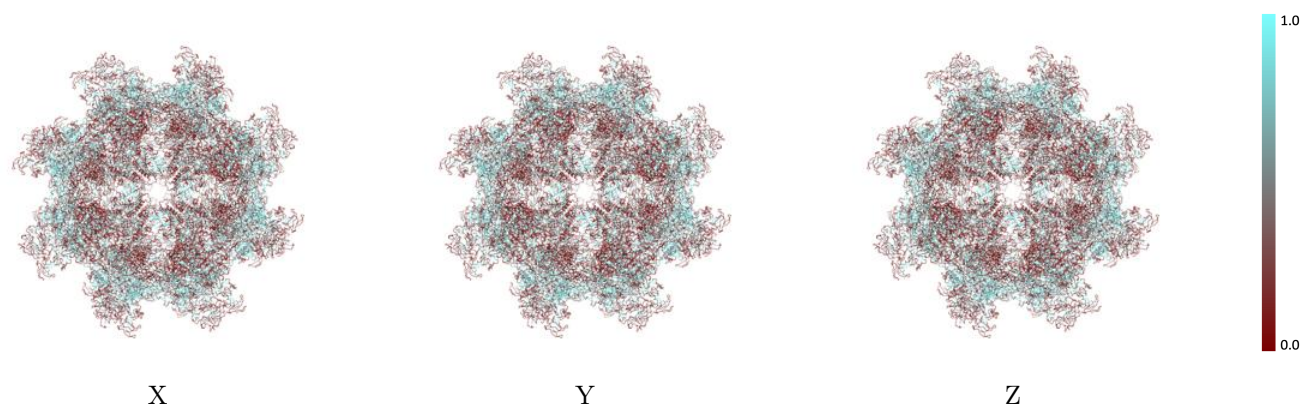
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



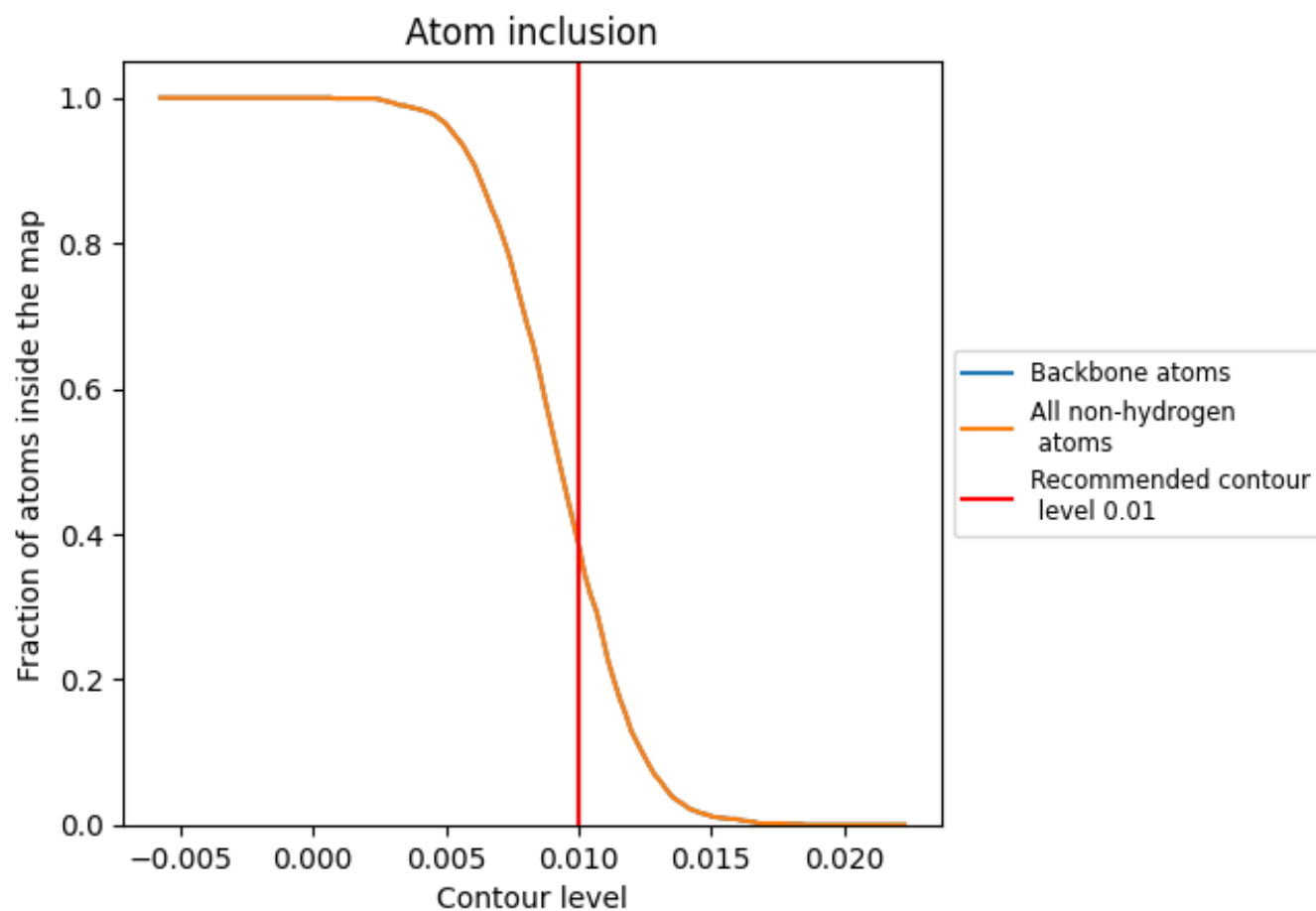
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 39% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3870	 0.1860
A000	 0.4890	 0.2080
A001	 0.4890	 0.2160
A002	 0.4890	 0.2130
A003	 0.4890	 0.2120
A004	 0.4890	 0.2180
A005	 0.4890	 0.2120
A006	 0.4890	 0.2130
A007	 0.4890	 0.2190
A008	 0.4890	 0.2130
A009	 0.4890	 0.2160
A010	 0.4890	 0.2180
A011	 0.4890	 0.2150
A012	 0.4890	 0.2120
A013	 0.4890	 0.2160
A014	 0.4890	 0.2110
A015	 0.4890	 0.2190
A016	 0.4890	 0.2160
A017	 0.4890	 0.2140
A018	 0.4890	 0.2130
A019	 0.4890	 0.2160
A020	 0.4890	 0.2130
A021	 0.4890	 0.2140
A022	 0.4890	 0.2090
A023	 0.4890	 0.2100
B000	 0.4040	 0.1840
B001	 0.4040	 0.1830
B002	 0.4040	 0.1820
B003	 0.4040	 0.1800
B004	 0.4040	 0.1780
B005	 0.4040	 0.1820
B006	 0.4040	 0.1790
B007	 0.4040	 0.1880
B008	 0.4040	 0.1800
B009	 0.4040	 0.1830



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
B010	0.4040	0.1880
B011	0.4040	0.1780
B012	0.4040	0.1780
B013	0.4040	0.1870
B014	0.4040	0.1810
B015	0.4040	0.1860
B016	0.4040	0.1810
B017	0.4040	0.1840
B018	0.4040	0.1790
B019	0.4040	0.1750
B020	0.4040	0.1830
B021	0.4040	0.1800
B022	0.4040	0.1810
B023	0.4040	0.1860
C000	0.4850	0.2110
C001	0.4850	0.2130
C002	0.4850	0.2200
C003	0.4850	0.2200
C004	0.4850	0.2150
C005	0.4850	0.2090
C006	0.4850	0.2200
C007	0.4850	0.2090
C008	0.4850	0.2160
C009	0.4850	0.2100
C010	0.4850	0.2090
C011	0.4850	0.2160
C012	0.4850	0.2170
C013	0.4850	0.2070
C014	0.4850	0.2160
C015	0.4850	0.2120
C016	0.4850	0.2120
C017	0.4850	0.2100
C018	0.4850	0.2120
C019	0.4850	0.2150
C020	0.4850	0.2150
C021	0.4850	0.2210
C022	0.4850	0.2220
C023	0.4850	0.2130
D000	0.1990	0.1220
D001	0.1990	0.1280
D002	0.1990	0.1250
D003	0.1990	0.1190

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
D004	0.1990	0.1250
D005	0.1990	0.1250
D006	0.1990	0.1220
D007	0.1990	0.1320
D008	0.1990	0.1350
D009	0.1990	0.1340
D010	0.1990	0.1330
D011	0.1990	0.1390
D012	0.1990	0.1290
D013	0.1990	0.1310
D014	0.1990	0.1300
D015	0.1990	0.1260
D016	0.1990	0.1320
D017	0.1990	0.1280
D018	0.1990	0.1260
D019	0.1990	0.1240
D020	0.1990	0.1210
D021	0.1990	0.1280
D022	0.1990	0.1190
D023	0.1990	0.1220
E000	0.1570	0.1390
E001	0.1570	0.1420
E002	0.1570	0.1450
E003	0.1570	0.1370
E004	0.1570	0.1400
E005	0.1570	0.1420
E006	0.1570	0.1410
E007	0.1570	0.1510
E008	0.1570	0.1350
E009	0.1570	0.1480
E010	0.1570	0.1430
E011	0.1570	0.1400
E012	0.1570	0.1320
E013	0.1570	0.1470
E014	0.1570	0.1360
E015	0.1570	0.1370
E016	0.1570	0.1420
E017	0.1570	0.1380
E018	0.1570	0.1400
E019	0.1570	0.1340
E020	0.1570	0.1370
E021	0.1570	0.1420

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
E022	0.1570	0.1350
E023	0.1570	0.1400
F000	0.1570	0.1400
F001	0.1570	0.1400
F002	0.1570	0.1430
F003	0.1570	0.1390
F004	0.1570	0.1320
F005	0.1570	0.1320
F006	0.1570	0.1360
F007	0.1570	0.1460
F008	0.1570	0.1360
F009	0.1570	0.1460
F010	0.1570	0.1370
F011	0.1570	0.1380
F012	0.1570	0.1300
F013	0.1570	0.1430
F014	0.1570	0.1380
F015	0.1570	0.1340
F016	0.1570	0.1430
F017	0.1570	0.1380
F018	0.1570	0.1330
F019	0.1570	0.1320
F020	0.1570	0.1410
F021	0.1570	0.1370
F022	0.1570	0.1350
F023	0.1570	0.1400